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Om nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:46:58 ; Search time 226 Seconds
 (without alignments)
 7833.856 Million cell updates/sec

Title:	US-10-812-387-1
Sequence:	1 catatgtgcacaaaggcttac.....atgagacttaattaaaggatcc 996
Scoring table:	IDENTITY_NUC
Score:	Gapop 10.0 , Gapext 1.0
Searched:	1303057 seqs, 888780828 residues
Total number of hits satisfying chosen parameters:	2606114
Minimum DB seq length:	0
Maximum DB seq length:	200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/podata/1/ina/1-COMB.seq: *
 2: /cgn2_6/podata/1/ina/5-COMB.seq: *
 3: /cgn2_6/podata/1/ina/6A-COMB.seq: *
 4: /cgn2_6/podata/1/ina/6B-COMB.seq: *
 5: /cgn2_6/podata/1/ina/H-COMB.seq: *
 6: /cgn2_6/podata/1/ina/PCUTUS-COMB.seq: *
 7: /cgn2_6/podata/1/ina/PP-COMB.seq: *
 8: /cgn2_6/podata/1/ina/RE-COMB.seq: *
 9: /cgn2_6/podata/1/ina/backFiles1.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	159	16.0	990	3 US-09-710-279-413
2	159	9.6	3	US-09-710-279-421
3	159	16.0	2975	3 US-09-710-279-3345
4	159	16.0	4114	3 US-09-710-279-4184
5	146	14.7	11466	3 US-09-956-171B-444
6	146	14.7	11466	3 US-09-781-9860-444
7	95.4	9.6	987	3 US-09-134-000-838
8	82.6	8.3	978	3 US-09-107-532A-366
9	47.8	4.8	400	3 US-09-956-171B-3720
10	47.8	4.8	400	3 US-08-781-9860-3720
11	3.9	7.218	2	US-08-232-463-14
12	37.4	3.8	10740	3 US-09-945-016-14834
13	36.4	3.7	61663	3 US-09-453-702B-62
14	36.4	3.7	61663	3 US-10-114-10-62
15	34.4	4429	3	US-09-455-486-7
16	34.2	3.4	2067	3 US-09-108-194-11
17	3.4	3.0	1539	3 US-09-621-916-15639
18	3.4	3.0	1083	3 US-09-134-000-22381
19	33.4	295	3	US-09-313-2943-5605
20	33.2	872	3	US-09-270-767-25560
21	33.2	2228	3	US-09-270-767-10203
22	3.3	2460	3	US-08-952-365-1
23	33.2	3.3	6065	3 US-09-800-729-35
24	33.2	3.3	101011	3 US-09-945-1616933

ALIGNMENTS

RESULT	US-09-710-279-413
;	Sequence 413, Application US/09710279
;	PATENT NO. 670492
;	GENERAL INFORMATION:
;	APPLICANT: KIMMELER, WILLIAM JOHN
;	TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
;	FILE REFERENCE: PUS480US
;	CURRENT APPLICATION NUMBER: US/09/710,279
;	PRIOR APPLICATION NUMBER: 60/164,258
;	PRIOR FILING DATE: 1999-11-09
;	NUMBER OF SEQ ID NOS: 472
;	SOFTWARE: PatentIn Ver. 2.1
;	SBO ID NO: 413
;	TYPE: DNA
;	ORGANISM: Artificial Sequence
;	FEATURE:
;	OTHER INFORMATION: Description of Artificial Sequence: synthetic
;	OTHER INFORMATION: nucleic acid sequence
;	US-09-710-279-413
;	QUERY MATCH
;	Best Local Similarity 16.0%; Score 159; DB 3; Length 990;
;	Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
Qy	2 ATATGTGCAACGCTTACATGGAACTGCTGACCGTAACTGTTAGAACAA
Db	8 ATATGTGCAACGCTTACATGGAACTGCTGACCGTAACTGTTAGAACAA
Qy	62 TGGATTTCGATTCAGCTGGACAGAGGTGATCTATCGCGCCGTTACAGCTGGA
Db	68 TGGACTTGCAATTATGGTATGCCAACCATGTTCCACGCCCCATTACACTACC
Qy	122 ACAGTGTGAGCTTACGGGAGGCCATCAGACAGTAGCTGCGTTATCGTATGGGAGA
Db	128 ATTGTGATCTGATTCAGCATCGATCGTCCTT--GATATGTTGTTGCGAACATTAA
Qy	182 ACTTGGAATATTATGGCAGCGATTATGAAAGCGTTATCTGTCGGGCC
Db	185 AGTAGGAGCTGATAGAATGCGATGTTAGCTTACGAA
Qy	242 TTATTCGCGCTATCGGGAGATACGGCACATG
Db	245 ATTAATGCTGAGCTATACAGTACCCATAGCTGTTAGTTACTAG

QY 302 TCCCCATGAGTTCTGACATGGGTCTGTCAGCTGTCAGCTTGGAAGACAAAG 361
Db 305 CACTGAGGTTTATGTTGGGTTAGGTTAATAAGATTAAGCTTACGGTAAC 364
QY 362 AAAGATGATGATCTTAAGATGAGAAGAAATTAGATCATTTGGAATCACTTC 421
Db 365 AAGAGTTAGAAATCAATTTATGAACTGAAAAAATACGACTTGTGAACTTC 424
QY 422 CGCTCACTGGATATGTCGACCGAACGGCCGAAACTTGACGATAGAACAGAG 481
Db 425 CTTPACATTCATGTTGACTGATGAAACAGGACATACCGCATAGACCTCAC 484
QY 482 ACGGCCTCAAGTCATGATATCACACCTGGGTCTGAGAACAGCCCACCTTAT 541
Db 485 CTTPACATTCATGTTGACTGATGAAACAGGACATACCGCATAGACCTCAC 544
QY 542 GCGATGTAACCAATGCAAGCAATTACAGGAATGACGGATGACGGACAAAG 601
Db 545 GGCATCTATCACTTAAGAAATACGCTTTAACGCCACAGAAATCAGCTAC 604
QY 602 AGATGGGCGGATTAAGCCCTCTGCTTGGCCAGGCTTAGGAACTGTGCGGG 661
Db 605 TAATGGTAAAGTGCTAGATGATCATGATCATGCTGGAAGAACATGGTACCG 664
QY 662 GGGATATACGGCCTCCGGTTGTCAGAGCTTGTGAAAGAACATCTAGAGC 721
Db 665 GTGGTTATGCTCACAGATGTTTATAGCGCTACATATTAGACCAACTACGT 724
QY 722 CGGCGGCCGAAACGAAGGTGTAACCGCGCTTCAATTGGCAATATGACGA 781
Db 725 GTTCCATAATGAGTGAATTATGAAATTGTTAAAGTCTAGATCAGTCAGTA 784
QY 782 TACCAAAGGGCGACTGATAAGGAGAGAACGAAATTCTATAGCCTATCTCG 841
Db 785 TCCCTCAAGGTGCACTT--CGATGCCATAATACATCACACATATCATTAG 841
QY 842 TGATGCAACGAAACTGGAAACTACTATTCACCATGACATCGCAATCCAA 901
Db 842 TGATGGAAGTAAAGAAAGGTTTATTAAGCCTTACTTAGCAATCAAATTCA 901
QY 902 AGTAAATTATTTCATGA 920
Db 902 AAATAAAATTAACTGAGA 920

RESULT 2

US-09-134-001C-2421
Sequence 2421, Application US/09134001C
; Patent No. 6380370
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; FILE REFERENCE: GTC-007
; CURRENT APPLICATION NUMBER: US/09/134, 001C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/064, 964
; PRIOR FILING DATE: 1997-11-08
; PRIOR APPLICATION NUMBER: US 60/055, 779
; PRIOR FILING DATE: 1997-08-14
; NUMBER OF SEQ ID NOS: 5674
; SEQ ID NO 2421
; LENGTH: 996
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2421

Query Match 16.0%; Score 159; DB 3; Length 996;
Best Local Similarity 49.8%; Pred. No. 1.4e-39;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGGCACAGCTTACATGAGAAGCTGTGACCTTAACGATTAAGGACAA 61

Db 14 ATATGGTACTGCCATTCTTATAGAAACACGTACCAATTAGCTAGACAA 73
QY 62 TGGATTGCAATTCAAGCTGGGACAGGGTGTCTATCGGGGTTAGCTGGA 121
Db 74 TGGACTTGCAATTGAAATTGTTAACTGTTACCGCACTTGTTCACGCCATTACACC 133
QY 122 ACATGAACTGAGGGGCCATGACACAGTAGGGTTATGGTATGGGAGAA 181
Db 134 AATTGACTAGTTGAGCTACGATCGCTCTT--GAATAGGTTGTTGAACTTAA 190
QY 182 AACITGGAAATAATTATGCGGACGCGCATTATGAAAGCGGTTATCTGCGGGC 241
Db 191 AATGGAGGTTATAGATTTGGTGTGTTAGGTTATAACGAAAGTTACGTTGAAAC 250
QY 242 TTATTTCCGGCTATCGGACTACGAAAAAGATGGGAGATCCGGTACATRG 301
Db 251 ATTACATCTGGAAACGCTCAACTACCTACACATACAGTATGGTATTAACTAG 310
QY 302 TCCCGATAGTTGACATGGGCTGTCAGCTGTCAGCTTGGAGACGTAAMAG 361
Db 311 CACCTGAGGTTTATGTTGGTTTAATTAAGTATTAGCGGAATTAAC 370
QY 362 AAAGATGATCCTTAAGATGTTAGGAAATATGATCTATGGATACGTTTAC 421
Db 371 AAAGGTTAGAAATCAATATGATGAAAAAATAGACTTTGAAATGTTCC 430
QY 422 CGCTCACTGGATATGTCAGACGGGCGAACCTGAGATAGAACAGAG 481
Db 431 CTTPACATTCATGTCATGTCATGTCAGTCAAAAGGACATACGGTACGCTCACATG 490
QY 482 ACGGCCTAACGCTATTAATCACCTGGCTCATGCAAGACGCCACCTTAT 541
Db 491 GCTTATTAACTGTTAAAGATAATTATGTCATACCTTAACTGAACTTAATTAGATT 550
QY 542 GGATGTAACCAATGTCAGCAATAGAGGAATAGGACATACGGTACGCTCACATG 601
Db 551 GGATCTACTAACTTAACTGAAATTACGGTTTAAACCCACAGAACTACAT 610
QY 602 AGATGGCGGATTAAGCCCTCTGCTTGGCCAGGCTTAGGAACTGTGGCTGCCG 661
Db 611 TAATGGTAAAGTGCTGTTAGATCAATGGCTGTGAACAGGACAAATGGCTACCG 670
QY 662 GGGATATACACCCCTTCCGGTTGTCAGAGCTGTTTAAACGAAACATCTAGASC 721
Db 671 GTGGTTATGCTCACAGATCGTTATAGCGCTACATATTAGACACCACTACGT 730
QY 722 CGGCGGCCGAAACGAAGGGTAAACGGCGTTCAATTGCGAAATATGACGA 781
Db 731 GTTCCATAATGAGTGAATTATGAAATTGTCAGAGCTGTTTAAAGTCTGAACT 790
QY 782 TACCAAAGGGCGACTGATAAGGAGAGAACGAAATTCTATAGCCTATCTCG 841
Db 791 TCCCTCAAGGTGCACTT--CGATGCCATAATACATCACACATCAATG 847
QY 842 TGATGCAACGAAACTGAAACTACTATTCACCATGACATCGCAATCCAA 901
Db 848 TGATGGAAGTAAAGAAAGGTTTATTAAGCCTTACTTAGCAATCAAATTCA 907
QY 902 AGTAAATTATTTCATGA 920
Db 908 AAATAAAATTAACTGAGA 926

RESULT 3

US-09-710-279-3345/C
Sequence 3345, Application US/09710279
; Patent No. 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMELLY, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERmidis NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: P3340US
; CURRENT APPLICATION NUMBER: US/09/710, 279
; CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164, 258
; PRIORITY FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 3345
; LENGTH: 2975
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-710-279-3345
; Query Match Similarity 16.0%; Score 159; DB 3; Length 2975;
; Best Local Similarity 49.8%; Pred. No. 2. 5e-39;
; Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
; Qy 2 ATATGTCGACAGCTTACATGGAAACTCTGACCGAACATGATAGCAGAACAA 61
; Db 1755 ATATGTCGACTGCCATTCTTATACAAACAGCTTACATGGTAGCAGAACAA 61
; Qy 62 TGGATTGCAATTCTAGCTGGCGACAGGTGTTCTCATCGCGCCGTACAGCTGA 121
; Db 1695 TGGATTGCAATTCTAGCTGGCGACAGGTGTTCTCATCGCGCCGTACAGCTGA 1696
; Qy 122 ACAGTGANGTGAGGGGGCATCAGCACAGTACCGTTATCGGTATGGGAGAA 181
; Db 1635 AATTGTGATCTAGATTCTAGAATGCTT--GAAATGGTTTGTGGAACAAATTAA 1579
; Qy 182 AACCTGGAAATAATTGGCCAGGAAATTGAAAGGATAGGGATACGGTACATTCGAAAC 241
; Db 1578 AACTGGACATTGAAATTGGCCAGGAAATTGAAAGGATAGGGATACGGTACATTCGAAAC 1519
; Qy 242 TTATTTCGGGAACTATGGCTAGAAGAAACGATAGGGATACGGTACATTCGAAAC 301
; Db 1518 ATTTCTACTGAAATTGGCTAGAAGAAACGATAGGGATACGGTACATTCGAAAC 1459
; Qy 302 TCCCGCATGAGTTGTGACATGGGTGCTAGCTGTCAGCTTGGAGAGCTAAAG 361
; Db 1458 CACCTGAGGAGGTTATTGTTGGTTTAATAAAGTATAGCGGAAATTAAAC 1399
; Qy 362 AAAGATTCGATTTAACGTTAGAGAAATTGATCTATGGATACGGTTAC 421
; Db 1398 AAAAGGTTAACGAAATCATTATPATGATGAAAAATTACGATTTGGATATGGTCTC 1339
; Qy 422 CGCTTCACTGATATTGTCAGACGGGACGGCGGAACCTGGCATAGAACAGACAG 481
; Db 1338 CTTTACATTCTAGTCAGTGCAGAACAGGATACGGCATACCTCACATG 1279
; Qy 482 AGGGCCTCAAAGTCATGATANTCAACTGGTCATGACGACAGGGCGCTTAT 541
; Db 1278 GCTTATTATAGTAAAGATAATTATGTTCTACCTTAACAAATGACCTAAATT 1219
; Qy 542 GGATGTCACATCTGGCGATATAAGGATCAGCGAGGAAATTGAGCAAG 601
; Db 1218 GECATCTATCTTAACTTAAGAAATTACGTTTTAACCCACGAAATCAACATCAAT 1159
; Qy 602 AGATGGCGGATAGCCCTTCTGCTTGTGCGCAGGTTGAACTGTTGGCTCGGG 661
; Db 1158 TATAGTAACTGTTAGTAGATCAATGGTGTGAGGAGAACATGTTAC 1099
; Qy 662 GGGATATACAGCGCTTCCCGTTCTGAGACTGTTATTGAGAAACATCTGAGC 721
; Db 1098 GCTGTTATGCTAACAGATCGTTTATACGGCTACATATTAAAGCACCTAGCT 1039
; Qy 722 CGCGGAGGATAAAGGATCAGCGCCATTCAATTGGCGAAATATGAG 781
; Db 1038 GTTCCCTAAATGAGATGAAATTGATGTTAACGTTCTAGAATCTGAGTA 979
; Qy 782 TACCAAGGGGAGTACCGAGAGCAATTCATATACCGAAATACTCCG 841
; Db 978 TCCCTGAGGCGAGTAT--CGATCCAAATACATACGACAAATCAATTAGG 922
; Qy 842 TGATGTGCGACGAAACTGAACTACTATTCCACCCTATGACAATCGCAATCCAA 901
; Db 921 TGATGGAAAGTAAAGAGAAAGTATTATTAAGCCCTACTTGTGACATCAATTCA 862
; Qy 902 AAGTAATTATTTCAGAA 843
; Db 861 AATTAAATTAACTGAGAA 843
; RESULT 4
; Sequence 4184, Application US/09710279
; PATENT NO: 6703492
; GENERAL INFORMATION:
; APPLICANT: KIMMELER, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PIJ480US
; CURRENT FILING DATE: 2000-11-09
; PRIOR FILING NUMBER: US/09/710,279
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO: 4184
; LENGTH: 4114
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; US-09-710-279-4184
; Query Match Similarity 16.0%; Score 159; DB 3; Length 4114;
; Best Local Similarity 49.8%; Pred. No. 2. 9e-39;
; Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
; Qy 2 ATATGTCGACAGCTTACATGGAAACTCTGACCGAACATGATAGCAGAACAA 61
; Db 1626 ATATGTCGACTGCCATTCTTATACAAACAAACCTTACATTATGGTAGAACAA 1685
; Qy 62 TGGATTGCAATTCTAGCTGGGACAGAGGTGTTCTACCGCGCTTACAGCTGGA 121
; Db 1686 TGGATTGCAATTCTAGCTGGGACAGAGGTGTTCTACCGCGCTTACAGCTGGA 1745
; Qy 122 ACAGTGAGCTAGGAGGCGCCATGACAGCACAGTACGGCTTATGGTATGGGAGAA 181
; Db 1746 AATTGTGCTAGTCACTGACATCGCTT--GAAATGGTTTGTGGAACAAATTAA 1802
; Qy 182 AACCTGGAAATAATTGGCCAGGAAATTGAAAGGATAGGGATACGGTACATTCGAAAC 241
; Db 1803 AAGTAGGAGCTTATAGATTTGGTGTGATGTTAAACGAAAGGTTGGCTTACGAC 1862
; Qy 242 TTATTTCGGCTATGGGAGTACGGAAACGATACGGGAGTACCGTACATTCGAAAC 301
; Db 1863 ATTTCTACTGTCAGCTGAGGAAATTGATCTATGGTACAGTTTACTTAG 1922
; Qy 302 TCCCGCATGAGTTGTCAGCTGAGGAAATTGATCTATGGTACAGTTTACTTAG 361
; Db 1923 CACCTGAGGAGCTTATGGTGTGTTAGTTAAAGATATAGCGAAATTAAAC 1982
; Qy 362 AAAGATTCGATCTTACGATGAGAAATTGATCTATGGTACAGTTTACTTAG 421
; Db 1983 AAGAGGTTAACGAAATTGATCTATGGTACAGCTGAGGAAATTGATCTGTCCTC 2042
; Qy 422 CCCTCTCTGCTGATATTGTCAGCCGCGCGCGAACCTGAGCTGAGGAAACAGCG 481
; Db 2043 CTTACTTCTGCTGACCTGAGGAAATTGATCTATGGTACAGCTGAGGAAACCTCAGAT 2102
; Qy 482 AGGGCCTCAAAGTCATGATANTCAACTGGTGTGAGCAGCCCCGACTTTAT 541
; Db 2103 GCTTATTATGTTAAAGATAATTGTCATACCTTACAAATGAACTTAATTAGG 2162
; Qy 542 GGCATGTAACCAATCTGCAGCAATAACAGGAAATCAGACCGAAAGCAATTAGAGGAGCAAG 601

Db 2163 GGCATCTATCTACTTAAGAATTACGCTTTAACGCCAACAGAAATCACCATACT 2222

Qy 602 AGATGGCGGATTAGCCCTTCGTGTTGGCCAAGGCTTAGGAACGTGTGCTGCCG 661

Db 2223 TAATAGGTAAAGTGTAGTAAAGTCATGGCTGAGCAGAACATGCTTACCG 2282

Qy 662 GGGGATTATACCCGCCTTCCGGTGTGAGCAGCTTATTGAAAGAACATCTAGGC 721

Db 2283 GTGGTTATACGTCAACAGATGGTTATACCGCTACATATTAGACACCAACTACGT 2342

Qy 722 CGGGGCCGATGAAACGGAAGGTTACAGCGCTTCAATTGGCAGAACATGCTTACCG 781

Db 2343 GTTCCCATATGAGATGAAATTATGATGTTAAAGTGTCTAGATCAGTCAGTA 2402

Qy 782 TACCAAGGGCCAGTGATAACGGAGAAGCAGAACATTCTATAGCAATATCTCG 841

Db 2403 TCCCTCAAGSTGCAATTAAATACATACACATATGATGTTGGCAGATAATGACCA 2459

Qy 842 TGATGCGAACGAAACTGGAAACTACTATTCACCACTATGACATCGCAAATCCAA 901

Db 2460 TGATGCGAACGAACTGGAAACTACTATTCACCACTATGACATCGCAAATCCAA 2519

Qy 902 AAGTAATTATTCTGAGA 920

Db 2520 AAATAAAATTACTGAGA 2538

RESULT 5
US-08-956-171E-444C Application US/080956171E

; Sequence 444, Application US/080956171E

; Patent No. 6593114

; GENERAL INFORMATION:

; APPLICANT: Charles Kunsch

; Gil H. Choi

; Patrick S. Dillon

; Craig A. Rosen

; Steven C. Barach

; Michael R. Fanion

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

; ADDRESSEE: Human Genome Sciences, Inc.

; STREET: 9410 Key West Avenue

; CITY: Rockville

; STATE: Maryland

; COUNTRY: USA

; ZIP: 20850

COMPUTER READABLE FORM:

; MEDIUM TYPE: DISKETTE, 3.50 inch, 1.4Mb storage

; COMPUTER: HP Vectra 486/33

; OPERATING SYSTEM: MS/DOS version 6.2

; SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/956,171E

; FILING DATE: 20-OCT-1997

; CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 60/009, 861

; FILING DATE: January 5, 1996

; APPLICATION NUMBER: 08/781, 986

; FILING DATE: January 3, 1997

; ATTORNEY/AGENT INFORMATION:

; NAME: Mark J. Hyman

; REGISTRATION NUMBER: 46, 789

; REFERENCE/DOCKET NUMBER: PB248P1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (240) 314-1224

; TELEFAX: (301) 309-8439

; INFORMATION FOR SEQ ID NO: 444:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 11466 base pairs

; TYPE: nucleic acid

STRANDEDNESS: double

SEQUENCE DESCRIPTION: SEQ ID NO: 444:

; US-08-956-171E-444

; Query Match 14.7%; Score 146; DB 3; Length 11466;

; Best Local Similarity 47.5%; Pred. No. 6 3e-35; Mismatches 515; Indels 3; Gaps 1;

; Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

; Db 3688 ATGTCACAGGATCAGATACAACTTAATAATCAGTACTCTTGACGACAG 3629

; Db 64 GATTGCAATTCTGCTGGCGACAGAGTGATCTCTTCGGCCGTACACTG 123

; Db 3628 GATTGATTTATCCATTGATGTCGAGCTGAGCCTGAGAAATATCGTTG 3569

; Qy 124 AGTGGAGCTGACGGAGGCCATCAGACAGACAGAGGTTATGGATGGAGA 183

; Db 3568 TCTTCGACTTGCCTGGCGACAGGAGATGTCGAGCAGACAGACAG 3512

; Qy 184 CTGGAAATATATATTGTCGAGGCTTAMGAAACGGTTATCTGGCTTATGG 243

; Db 3511 ATGGAGGTATTATATGGTTAATGAGACATGGCTGCGTGGATCAC 3452

; Qy 244 TATTTCGAGGTTATAGTCATATGTCACACACAAAGGGAGCTACCTTC 303

; Db 3451 TATTTCGAGGTTATAGTCATATGTCACACACAAAGGGAGCTACCTTC 3392

; Qy 304 CGCGATGAGTTGACATGGCTGCTGAGTCAGTGTGCTTGGAGCTAAAGA 363

; Db 3391 CAATATGAAATTGGACATAGTGGATATGAGATATGAACTGAACT 3332

; Qy 364 AAGATTCGATCTTACGATGAGAAAATTAGTCATATGGATACAGTTACCG 423

; Db 3331 CAAGATCCAAATCAGTGTGAGCTTATTAATGACATGGCTGAGTCGG 3272

; Qy 424 CTTCACTGGATATGTCAGACCGCGGCGCGAACCTGAGATAAGGAGCAG 483

; Db 3271 TTGCATTATCATGTTTCGATGCACTGACATACAGTCGAGTTCTATTAA 3212

; Qy 484 GGCTCAAGCTGATGAAATCACCTGGTGTGAGACACCCACTTATGG 543

; Db 3211 GAAGGGTTAAAGATAATCCATTGTCGATTCAGTAACTCATCCAGCTAAATGG 3152

; Qy 544 CATGTTACATCTGCAAGATACAGGATGACGGAGCAATTAGAGAAAG 603

; Db 3151 GATTATGAAATTAGACATATTCATATTCCTATCCGACAGCAATT 3092

; Qy 604 ATGGCGGATAGCCTTCTGCTTGGCCAAGGCTGGACTGTGCTCGCGGG 663

; Db 3091 TTGGAGGTGATGATGACCTTGTGACATGAGTCATTTGCACTGCGAGG 3032

; Qy 664 GATTTACATCCGGTTGAGCTGAGCTTATGAGAACTGCTTTC 723

; Db 3031 GGATTCTTCACTGGACCTTGTGAGATGCGCTTCAATTTGGCAATATGACGATA 2972

; Qy 724 GCGGCGATGAAACGAAAGGTTGACAGCGCTTTC 783

; Db 2971 AACATGATGAAATGGTTATGAGATGCTTATGAGATAATGGCTGAAATTA 2912

; Qy 784 CCAAGGGCCAGTGTAGGAGAACATTCATTACCGATACTTCGGTG 843

; Db 2911 CGATGAGTTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTGAGCTG 2852

; Qy 844 ATGTCACAGGATCAGATACAACTTAATAATCAGTACTCTTGACGACAG 903

; Db 2851 ATAATTTAACTACAGAAGCTTATGAGTTATGGCTGAGCTGAGTTAGTAGCA 2792

; Qy 904 GAAATTTATTCATGAGACCTGACTGTTGGACCTAAAGCTTTCGCTAAAGA 963

; Db 2791 TTAAGCTCAGGATTTATGAAAGATGAGGATTATGAGCTGAGGAG 2732

STATE: Massachusetts
COUNTRY: USA
ZIP: 02334
COMPUTER READABLE FORM:
COMPUTER: PC
MEDIUM TYPE: CD/ROM ISO9660
OPERATING SYSTEM: <Unknown>
SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/107,532A
FILING DATE: 30-Jun-1998
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 60/085,998
FILING DATE: 14 May 1998
FILED: 14 May 1998
APPLICATION NUMBER: 60/051571
FILING DATE: July 2, 1997
TELEFAX: (781)893-9277
ATTORNEY/AGENT INFORMATION:
NAME: Arinello, Pamela Dencke
REGISTRATION NUMBER: 40,489
REFERENCE/DOCKET NUMBER: GTC-012
TELECOMMUNICATION INFORMATION:
TELEPHONE: (781)893-5007
INFORMATION FOR SEQ ID NO: 366:
SEQUENCE CHARACTERISTICS:
LENGTH: 978 base pairs
TYPE: nucleic acid
STRANDBEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Enterococcus faecium
FEATURE:
NAME/KEY: misc feature
LOCATION: (B) LOCATION 1...978
SEQUENCE DESCRIPTION: SEQ ID NO: 366:

US-09-107-532A-366
Query Match 8.3%; Score 82,6; DB 3; Length 978;
Best Local Similarity 45.8%; Pred. No. 1..8-15; Indels 6; Gaps 2;
Matches 363; Conservative 0; Mismatches 424; Indels 6; Gaps 2;
QY 197 TATTCGGCGGCGTAAATGAAACCGGTATCTTGCGGGCGTTATTTCGGCT 256
Db 191 TTATTCAGCGACAAATGAAAGGATGGATGTTCAATTTTCGGT 250
QY 257 ATGGGGGTGACGAAGAACGATACGGGAGATACCCATCACATGCCGATGAGTT 316
Db 251 ATGCTGTTATAAGAA..ATACAAGAACGGAAGAACGAAATGATCTCTTTGAATT 307
QY 317 TGACATGGGTGCTGTGCTGTCAGTCAAGTCTTGAGAGCGTAAGAAGATGATCT 376
Db 308 TCCCTTGATTTAGGCAACTCTCAAGTAGGAGAAGCTAAATGTAAMATA 367
QY 377 TACAGTTGAGAGAAAATPAGATCTATGGATAGCTTACCGTTACTGGTAT 436
Db 368 TCAATTAGCAAAATAATTATAGTGTGACTTCCTTATCCCTTACATGGCT 427
QY 437 TGTCAAGCGGACGGCGAACACTTGCGATGAGAACAGAGAGGGCGTCAGAGCT 496
Db 428 TAGCTGT..AAAGAAATACTCAATTGCTGAGAGATGAGCTCATAT 484
QY 497 ATGATATCAACCTGGTGTCAATGAGCACAGGCCGCTTATGGCATGAACTAC 556
Db 485 ATGATACCTGGGGTCTTACCAATACTCTTATGGCTACATCAATTGAT 544
QY 557 TCCGACCATATCAGGATCACCGAGCAATTAGGAGCAAGAGATGGCGGATAG 616
Db 545 TAACAAATTATCGTGTCTATGGATGAACTCTCAAATAATTTCAAATCAAATTA 604
QY 617 CCCTTCTGCTTGGCCAAGGCTTAGGAACCTGCTGGCTCGGGGGATTACACCGC 676

RESULT 8
US-09-107-532A-366
Sequence 366, Application US/09107532A

Patient No. 658275
GENERAL INFORMATION:

APPLICANT: Lynn A. Doucette-Stamm and David Bush,
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310
CORRESPONDENCE ADDRESS:

ADRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 10 Beaver Street
CITY: Waltham

Best Local Similarity 48.1%; **Pred.** No. 0; **Mismatches** 147; **Indels** 0; **Gaps** 0
Matches 136; **Conservative** 0;

Sequence 14, **Application** US/08232463
Patent No. 5670367

GENERAL INFORMATION:
APPLICANT: DORRER, F.
APPLICANT: SCHIEFLINGER, F.
APPLICANT: PALMER, F. G.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS

NUMBER OF SEQUENCES: 52

CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
ZIP: 22313-0299

COMPUTER READABLE FORM:
MEDIA TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE:
APPLICATION NUMBER: EP 91 114 300.6
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE DOCKET NUMBER: 30472/114 IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEX: 899149
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: ptzgpt-F1s

RESULT 11
S-08-232-463-14/C

b 346 TTGGATACGTTTCACTTGTCGCCATGAGTTGACATGGCTGTGATGCTGTCAGCT 405
b 333 GACGGCGATGAACTATAGCCAAATGAAATTGTCAGATGGATATAACACAGC 274
b 213 ATGGATACGTTTACGCCCTACTGGATATGTCAGACGGGAGGGCGGAACCTGAC 465
b 466 ATAGAACCCAGAGCAGGGCTTAAGAGGTTGAAGGTGTTATAAAGATATTCCTATTGTCCTAACAT 94
b 153 GTTCAATTAAAGAGGGCTGAAGTGTATAAAGATATTCCTATTGTCCTAACAT 525
b 526 AGCCCCGACTTATATGCATGAAACCATCTGCAGGATATA 568
b 93 CATCCAGACTAAATGTCATATGATTAATGAGACATATA 51

y 214 ATTGAGATATGAAACAGACAGCATCCAAATACATGTTGAGCTGTATATTAAATGAC

RESULT 13
 US-09-453-702B-62/C
 Sequence 62, Application US/09453702B
 Patent No. 6365723
 GENERAL INFORMATION:
 APPLICANT: Blattner, Frederick R.
 Burland, Valerie
 Perna, Nicole T.
 Plunkett, Guy
 Welch, Rod
 TITLE OF INVENTION: No. 6365723el Sequences of *E. coli* 0157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch. 1.44MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/453, 702B
 FILING DATE: 03-Dec-1999
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 60/110, 955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-3166
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61663
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 62:
 ; US-09-453-702B-62:
 Query Match 3.7%; Score 36.4; DB 3; Length 61663;
 Best Local Similarity 49.5%; Pred. No. 5.7;
 Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 Qy 615 AGCCCTTCTGCTTGGCCAGGCCTAGAACGACTGTGGCTGGGGGATATAACAC 674
 Db 12938 AGCCCTTCTGCTTGGCCAGGCCTAGAACGACTGTGGCTGGGGGATATAACAC 674
 Qy 675 GCCTTCGGTTGTCAGAGCTGTATTGAAAGACATCTAGAGCGGGGGATGA 734
 Db 12878 CTCACTAAGATTTCATAGAAATCTCTTCTACTTCACTTCAGAACATTATGGTGA 12819
 Qy 735 AACGAAAGGTGTAACGCCCTTCAATTGGCAAATATGAGCATCCAAGGGCC 794
 Db 12818 ACTGAAAGTTTGCAAGTCCTTGTACTCATGGTCAGATGAAAGTGCGC 12759
 Qy 795 AGTGTAAAG 804
 Db 12758 AAAGGATTCG 12749

RESULT 14
 US-10-114-170-62/C
 Sequence 62, Application US/10114170
 Patent No. 6855814
 GENERAL INFORMATION:
 APPLICANT: Blattner, Frederick R.
 Burland, Valerie
 Perna, Nicole T.
 Plunkett, Guy
 Welch, Rod
 TITLE OF INVENTION: No. 6855814el Sequences of *E. coli* 0157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch. 1.44MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/114, 170
 FILING DATE: 01-APR-2002
 CLASSIFICATION: <Unknown>
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 09/453, 702
 FILING DATE: 03-DEC-1999
 APPLICATION NUMBER: 60/110, 955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 REFERENCE DOCKET NUMBER: 960296.95017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-9166
 TELEFAX: (608) 251-3166
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61663
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 62:
 ; US-10-114-170-62:
 Query Match 3.7%; Score 36.4; DB 3; Length 61663;
 Best Local Similarity 49.5%; Pred. No. 5.7;
 Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 Qy 615 AGCCCTTCTGCTTGGCCAGGCCTAGAACGACTGTGGCTGGGGGATATAACAC 674
 Db 12938 AGCCCTTCTGCTTGGCCAGGCCTAGAACGACTGTGGCTGGGGGATATAACAC 674
 Qy 675 GCCTTCGGTTGTCAGAGCTGTATTGAAAGACATCTAGAGCGGGGGATGA 734
 Db 12878 CTCACTAAGATTTCATAGAAATCTCTTCTACTTCACTTCAGAACATTATGGTGA 12819
 Qy 735 AACGAAAGGTGTAACGCCCTTCAATTGGCAAATATGAGCATCCAAGGGCC 794
 Db 12818 ACTGAAAGTTTGCAAGTCCTTGTACTCATGGTCAGATGAAAGTGCGC 12759
 Qy 795 AGTGTAAAG 804
 Db 12758 AAAGGATTCG 12749

RESULT 15

US-09-455-486-7/C

Sequence 7, Application US/09455486

Patent No. 6833438

GENERAL INFORMATION:

APPLICANT: Daniel E. Afar

APPLICANT: Rene S. Hubert

APPLICANT: Arthur B. Raitano

APPLICANT: Douglas C. Saffran

APPLICANT: Stephen C. Mitchell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

TITLE OF INVENTION: EXPRESSED IN HUMAN CANCERS AND USES THEREOF

FILE REFERENCE: 129-17-US-11

CURRENT APPLICATION NUMBER: US/09/455, 486

PRIORITY DATE: 1999-12-06

PRIORITY APPLICATION NUMBER: 09/323, 873

PRIORITY FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 7

LENGTH: 4429

TYPE: DNA

ORGANISM: Homo sapiens

FEATURE: CDS

NAME/KEY: (85) ... (1464)

LOCATION: US-09-455-486-7

Query Match 3.5%; Score 34,4; DB 3; Length 4429;

Best Local Similarity 51.3%; Pred. No. 6.2.; Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Oy 243 TTAATTCGGGATATGGCGAGTACGAAAAACCATACGGGAATACCGTTACATGT 302

Db 1726 TCAATCTACGCTCAATGGCTCTGGAAATAAGAGTCGGACCTGCACITCA 1667

Oy 303 CGCGCATGAGTTTGACATGGCTGCTGAGCTGTCTTGAGACCTAAAGA 362

Db 1666 CTAACCTGAGATAAAATGGGTTCTCCAGTAGTCAGTCATTCTCAAAGACAAGC 1607

Oy 363 AAAGATTCGATCTTAACGGTTGAGAAATT 398

Db 1606 AATGTTCCCTCACTCACGGTGTAAAGAAAACCT 1571

Search completed: March 18, 2006, 11:58:33
Job time : 228 Secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:52:29 ; Search time 992 seconds¹
 (without alignmentB)
 8302.722 Million cell updates/sec

Title: US-10-812-387-1
 Perfect score: 996
 Sequence: 1 catatggcacagtcac.....atggacttaattaaaggatcc 996

Scoring table: IDENTITY_NUC
 Gappp 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications NA_Main:*

1: /cgn2_6/podata/1/pbpna/us07_pubcomb.seq: *
 2: /cgn2_6/podata/1/pbpna/us08_pubcomb.seq: *
 3: /cgn2_6/podata/1/pbpna/us09a_pubcomb.seq: *
 4: /cgn2_6/podata/1/pbpna/us09b_pubcomb.seq: *
 5: /cgn2_6/podata/1/pbpna/us10a_pubcomb.seq: *
 6: /cgn2_6/podata/1/pbpna/us10b_pubcomb.seq: *
 7: /cgn2_6/podata/1/pbpna/us10c_pubcomb.seq: *
 8: /cgn2_6/podata/1/pbpna/us10d_pubcomb.seq: *
 9: /cgn2_6/podata/1/pbpna/us11a_pubcomb.seq: *
 10: /cgn2_6/podata/1/pbpna/us11b_pubcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query %	Match Length	DB ID	Description
1	996	100.0	996	9	US-10-812-387-1 Sequence 1; Appli Sequence 1719, Ap
2	439.8	44.2	990	3	US-09-914-300-1719 Sequence 9120, Ap
3	287.8	28.9	984	7	US-10-282-122A-9120 Sequence 9817, Ap
4	237.7	23.8	969	7	US-10-282-122A-9817 Sequence 9817, Ap
5	232.6	23.4	990	7	US-10-398-221-566 Sequence 766, App
6	232.6	23.4	990	7	US-10-398-221-566 Sequence 2682, Ap
7	232.6	23.4	990	7	US-10-398-221-566 Sequence 2682, Ap
8	173.8	17.4	1616	6	US-10-429-802-17 Sequence 17, Appli
9	173.8	17.4	1616	6	US-10-430-503-8 Sequence 8, Appli
10	160.2	16.1	978	7	US-10-282-122A-34300 Sequence 34300, A
11	159	16.0	996	7	US-10-724-972A-1455 Sequence 1455, Ap
12	146	14.7	993	7	US-10-282-122A-7960 Sequence 7960, Ap
13	146	14.7	11465	2	US-09-781-986A-444 Sequence 444, App
14	146	14.7	11466	7	US-10-329-624-444 Sequence 444, App
15	142.8	14.3	1002	3	US-09-815-242-8383 Sequence 8383, Ap
16	142.4	14.3	981	3	US-09-815-242-4665 Sequence 4665, Ap
17	117.8	11.8	972	7	US-10-282-122A-35759 Sequence 35759, Ap
18	95.4	9.6	972	7	US-10-282-122A-29096 Sequence 29096, A
19	80.6	8.1	972	7	US-10-282-122A-21716 Sequence 21716, A
20	80.2	8.1	2256646	7	US-10-470-565-1 Sequence 1, Appli
21	72.4	7.3	1050	7	US-10-282-122A-12199 Sequence 12199, A
22	63.6	7	1039	2	US-10-398-221-911 Sequence 911, App
23	63.6	6.4	978	7	US-10-398-221-8826 Sequence 2826, App

ALIGNMENTS

RESULT 1
 US-10-812-387-1
 ; Sequence 1, Application US/10812387
 ; Publication No. US20050114252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: SIVARAMAN, HEPHZIBAH
 ; APPLICANT: PUNDLE, ARCHANA VISHNU
 ; APPLICANT: SURISH, CHERAVAKATTU GOPALAN
 ; APPLICANT: DODSON, GEORGE GUY
 ; APPLICANT: BRANNIGAN, JAMES ANTONY
 ; TITLE OF INVENTION: PROCESSES FOR PRODUCTION OF LARGE AMOUNT OF PENICILLIN V
 ; TITLE OF INVENTION: PROCESSES FOR PRODUCTION OF LARGE AMOUNT OF PENICILLIN V
 ; FILE REFERENCE: 056859-0196
 ; CURRENT APPLICATION NUMBER: US/10/812,387
 ; CURRENT FILING DATE: 2004-03-30
 ; PRIOR APPLICATION NUMBER: PCT/IB03/06198
 ; NUMBER OF SEQ ID NOS: 1
 ; SOFTWARE: PatentIn Ver. 3.2
 ; SEQ ID NO: 1
 ; LENGTH: 996
 ; TYPE: DNA
 ; ORGANISM: Bacillus subtilis
 ; US-10-812-387-1

Query Match 100.0%; Score 996; DB 9; Length 996;
 Best Local Similarity 100.0%; Pred. No. 1; Mismatches 0; Indels 0; Gaps 0;

Matches 996; Conservative 0;

Sequence 1 CATATGGCACAGTCATGGAACCTGTGCAACCGTAAGTATAGTAAAGACA 60
 Sequence 2 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 3 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 4 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 5 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 6 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 7 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 8 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 9 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 10 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 11 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 12 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 13 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 14 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 15 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 16 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 17 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 18 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 19 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 20 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 21 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 22 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120
 Sequence 23 61 ATGGATTGCAATTCTAGTGGGACAGGGTTATCTCTATCGCGCGTTACAGCTG 120

181 AACCTGGAAATTATATTATGGCGACGCCATTATGAAAGCGCGTTACTTGCGGG 240
 181 AACCTGGAAATTATATTATGGCGACGCCATTATGAAAGCGCGTTACTTGCGGG 240

241 CTATTTTCCGCGCTATGGCGGAGAACGAGACGCGGAGAACGACCGTACACAT 300

Db 241 CTTTATTTCGGGCTATGGGGAGTAGAAACAGTACCGGAAGATACGGTCACATT 300

Qy 301 GRCGGCATGAGTTGTGACATGGCTGTCACTGCTGTCAGTCAGTCTGGAAAGCATAA 360

Db 301 GRCGGCATGAGTTGTGACATGGCTGTCACTGCTGTCAGTCAGTCTGGAAAGCATAA 360

Qy 361 GAAAAGATGCGATCTTAACGATGGAGAAAATTAGATCTTATGGATACAGTTA 420

Db 361 GAAAAGATGCGATCTTAACGATGGAGAAAATTAGATCTTATGGATACAGTTA 420

Qy 421 CGCCTCACTGGATATGTCAGCCGGACAGGAAACCTGAGTAGAACGATGAAAGCA 480

Db 421 CGCCTCACTGGATATGTCAGCCGGACAGGAAACCTGAGTAGAACGATGAAAGCA 480

Qy 481 GACGGCCCTCAAGCTATGTAATCAACCTGGTCATGACGAAAGCCCCACTTAA 540

Db 481 GACGGCCCTCAAGCTATGTAATCAACCTGGTCATGACGAAAGCCCCACTTAA 540

Qy 601 GAGATGGCGGATTAGCCCTTCGCTTGSACAGCTTGGAACTGTCGTCGCG 660

Db 601 GAGATGGCGGATTAGCCCTTCGCTTGSACAGCTTGGAACTGTCGTCGCG 660

Qy 661 GGGGATATAACGCCCTCCGGTTGGAGCTTGTAGAGCTCTAGAG 720

Db 661 GGGGATATAACGCCCTCCGGTTGGAGCTTGTAGAGCTCTAGAG 720

Qy 721 CCGGGGCGCATGARAGAGGGTAAAGCCGCTTTCGCTTGTGCAAGCTTGC 780

Db 721 CCGGGGCGCATGARAGAGGGTAAAGCCGCTTTCGCTTGTGCAAGCTTGC 780

Qy 781 ATCCAAAGGCCGATGAAACGGAAGGTTGTAACAGCCGCTTTCGCTTAC 840

Db 781 ATCCAAAGGCCGATGAAACGGAAGGTTGTAACAGCCGCTTTCGCTTAC 840

Qy 841 GTGATGTCGACGAAACTGGAAACTACTTTCCACCATGACAACTGGCAATCAA 900

Db 841 GTGATGTCGACGAAACTGGAAACTACTTTCCACCATGACAACTGGCAATCAA 900

Qy 901 AAGCTAAATTATTCATGAGACCTTGACTGTTGGACCTAAAGTGTTCGCTAA 960

Db 901 AAGCTAAATTATTCATGAGACCTTGACTGTTGGACCTAAAGTGTTCGCTAA 960

Qy 961 GCAGBAGAGGTATTCATGGCTTAATTAGGATCC 996

Db 961 GCAGBAGAGGTATTCATGGCTTAATTAGGATCC 996

RESULT 2

US-09-974-300-1719

Sequence 1719, Application US/09974300

Patent No. US20030146721A1

GENERAL INFORMATION:

APPLICANT: Berke, Randy M.

APPLICANT: Clausen, Ib Groth

TITLE OF INVENTION: Methods For Monitoring Multiple Gene

TITLE OF INVENTION: Expression

FILE REFERENCE: 1008_500-US

CURRENT APPLICATION NUMBER: US/09/974, 300

CURRENT FILING DATE: 2001-10-05

PRIOR APPLICATION NUMBER: 09/650, 598

PRIOR FILING DATE: 2000-10-06

PRIOR APPLICATION NUMBER: 60/279, 526

NUMBER OF SEQ ID NOS: 8481

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 1719

LENGTH: 990

TYPE: DNA

i ORGANISM: Bacillus licheniformis

US-09-974-300-1719

Query Match 44.2%; Score 439.8; DB 3; Length 990;

Best Local Similarity 65.3%; Pred. No. 1.5e-121; Mismatches 342; Indels 0; Gaps 0;

Matches 645; Conservative 0; Pred. No. 1.5e-121; Mismatches 342; Indels 0; Gaps 0;

Db 1 ATGTCGCAACTCTAACATGGAAACTGCTGACCGTAACATGATTTAGGAGACATG 63

Db 1 ATGTCGCAACTCTAACATGGAGACATGATTTAGGAGACATG 60

Qy 64 GATTTCGATTCAGCTGGGACAGGGATTCATCGCGCGCTTACGTCGAC 123.

Db 64 GATTTCGATTCAGCTGGGACAGGGATTCATCGCGCGCTTACGTCGAC 120

Qy 684 CITGGAAATATAATTGCGACGCACTTATGAAAGCCTTATCTGCGCGCTT 243

Db 684 CITGGAAATATAATTGCGACGCACTTATGAAAGCCTTATCTGCGCGCTT 240

Qy 124 ATGAACTGAGGGAGGGCCATCGACAGCAGTGGCTTATGGTATGGGAGAAA 183

Db 124 ATGAACTGAGGGAGGGCCATCGACAGCAGTGGCTTATGGTATGGGAGAAA 180

Qy 121 AGTGAAGGGAGGGAGGGAGCATGGGGCGGTATCGGATGGAGCTGGAG 180

Db 121 AGTGAAGGGAGGGAGGGAGCATGGGGCGGTATCGGATGGAGCTGGAG 180

Qy 184 CITGGAAATATAATTGCGACGCACTTATGAAAGCCTTATCTGCGCGCTT 243

Db 184 CITGGAAATATAATTGCGACGCACTTATGAAAGCCTTATCTGCGCGCTT 240

Qy 181 CTCAAGAATGCTGCTTGTGGATGTGTGATGAAAGATGCTGCTTGC 303

Db 181 CTCAAGAATGCTGCTTGTGGATGTGTGATGAAAGATGCTGCTTGC 300

Qy 244 TATTTCGGGCTATGGGAGTAGGAAAGGATAGGGAGATCGTCACATGTC 303

Db 244 TATTTCGGGCTATGGGAGTAGGAAAGGATAGGGAGATCGTCACATGTC 300

Qy 304 CGCATGATGTTGAGCATGGTGTGCTGTCAGCTGTCAGTGTGGATGGTGTG 363

Db 304 CGCATGATGTTGAGCATGGTGTGCTGTCAGCTGTCAGTGTGGATGGTGTG 360

Qy 361 CGGGCTTTCCATACGATGCTGCACTTGTGGATGTGGATGGAGCTGGCG 420

Db 361 CGGGCTTTCCATACGATGCTGCACTTGTGGATGTGGATGGAGCTGGCG 420

Qy 424 CTTCACTGGATTTGAGACGGACGGACGGAAACTGACATGACGACAGCAC 483

Db 424 CTTCACTGGATTTGAGACGGACGGACGGAAACTGACATGACGACAGCAC 480

Qy 484 GCGCTCAAGCTTGTGAACTGACCTGTCGTCAGTCGAGCAGCCGACTTATGG 543

Db 484 GCGCTCAAGCTTGTGAACTGACCTGTCGTCAGTCGAGCAGCCGACTTATGG 540

Qy 544 CATGATCCAACTCTGCGCAATACGGGATCTGAGGCAATAGGAGCAAGAG 603

Db 544 CATGATCCAACTCTGCGCAATACGGGATCTGAGGCAATAGGAGCAAGAG 600

Qy 541 CATTGACCAATGTCGCAACTTATGGCTCTGAGGGAGCATGTTGCCGCAAA 600

Db 541 CATTGACCAATGTCGCAACTTATGGCTCTGAGGGAGCATGTTGCCGCAAA 600

Qy 604 ATGGGGGAAATTGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGG 663

Db 604 ATGGGGGAAATTGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGG 660

Qy 601 ATGGGGGAAATTGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGG 660

Db 601 ATGGGGGAAATTGGCTCTGGCTTGGCTTGGCTTGGCTTGGCTTGG 660

Qy 664 GATTATCACCSCTTCCGGGTTGTTAGGCTTGTGGCTTGGCTTGG 723

Db 664 GATTATCACCSCTTCCGGGTTGTTAGGCTTGTGGCTTGGCTTGG 720

Qy 724 GCGCCGATGAAAGGGTGTACGCCGCTTAAATTGGGAAATGACATA 783

Db 724 GCGCCGATGAAAGGGTGTACGCCGCTTAAATTGGGAAATGACATA 780

Qy 721 GTGTCGCGATGAAACAGGAGGGCTCTCCGCTTGTGCTCTGATGAT 780

Db 721 GTGTCGCGATGAAACAGGAGGGCTCTCCGCTTGTGCTCTGATGAT 780

Qy 784 CCAGAGGGCGAGGATGAACTGGAGAACTTATGGCAATATCCCTG 843

Db 784 CCAGAGGGCGAGGATGAACTGGAGAACTTATGGCAATATCCCTG 840

Qy 844 ATGGCGCAACGAAACTGGAGAACTACTTTCCACCACTGACATGGGAAATCCAA 903

Db 844 ATGGCGCAACGAAACTGGAGAACTACTTTCCACCACTGACATGGGAAATCCAA 900

Qy 841 ATGGCGAGGGAGGTGCACTTATTCACCATGATTCACGAGTCAGTC 900

Db 841 ATGGCGAGGGAGGTGCACTTATTCACCATGATTCACGAGTCAGTC 900

Qy 904 GTAAATTGTTGATGAGACCTGAGCTTGGCTTAAGGGTTCCGCTAA 963

Db 904 GTAAATTGTTGATGAGACCTGAGCTTGGCTTAAGGGTTCCGCTAA 963

Qy 901 GTTGCTTATGACGAGACCTGAGCAACGAAATTAGGGCTTACGCCAAG 960

Db 901 GTTGCTTATGACGAGACCTGAGCAACGAAATTAGGGCTTACGCCAAG 960

Qy 964 GAAGAGGAGTTCGAGTTAA 990

Db 964 GAAGAGGAGTTCGAGTTAA 990

Db 961 GAGAGACGGTCATTCCTCAATCA 987 Qy 244 TATTTCCGCGCTATGGGGAGTACCAAALACGATAACGGAGATACCGTCACATGTC 303
 RESULT 3 ; Sequence 9817, Application US/10282122A
 US-10-282-122A-9120 ; Publication No. US20040029129A1
 Publication No. US20040029129A1 ; GENERAL INFORMATION:
 - APPLICANT: Wang, Liangsu
 - APPLICANT: Zamudio, Carlos
 - APPLICANT: Malone, Cheryl
 - APPLICANT: Haselbeck, Robert
 - APPLICANT: Ohlsen, Kari
 - APPLICANT: Zyskind, Judith
 - APPLICANT: Wall, Daniel
 - APPLICANT: Trawick, John
 - APPLICANT: Carr, Grant
 - APPLICANT: Yamamoto, Robert
 - APPLICANT: Forbyth, R.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/220,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/257,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 REMAINING PRIOR Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 7864
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 9120
 LENGTH: 984
 TYPE: DNA
 ORGANISM: *Bacillus anthracis*
 US-10-282-122A-9120

Query Match 28.9%; Score 287.8; DB 7; Length 984;
 Best Local Similarity 56.0%; Pred. No. 1.2e-75; Indels 0; Gaps 0;
 Matches 544; Conservative 0; Mismatches 427;

Qy 4 ATGGCACAGTCCTACATGGAACTGCGGACGTTAACATGTTATTGAGAACAGTCG 63 Db 301 CCATTGAGTTGTACTGGAGTCAATCCTGTCAGACAACTGTCAGGTTAAGAAA 360 Qy 304 COGCMAGAGTTGTGACCATGGTCTGTCACTTGCGAAGAGTAAAGAA 363 Db 364 AAGATTCGACCTTAACGATGTTGAGAGAAAATTGAGCTATGGATCAGTTAACCG 423 Qy 361 TCTGTTAGATGCAATACCTTTGGATATACCCATTACCGGATTAGGACTTACCG 420 Db 424 CTTCACCTGGATATTCAGACGGAGGGCGAGAACTGACGATAGACAGAGAC 483 Qy 421 CTACATGCAATTAGGGATAATGGCGAGATTCATGGTACTGGATCCAGATGAA 480 Db 484 GGCCCTCAAACCTCTATGATATCAACCTGGTCTGAGTACCGCCACTTTATGG 543 Qy 481 GGATTAATGATGATAACCACTAGGAGTGTGACGATAGTCGGAGTTAATGG 540 Db 544 CATGAAACATCTGGAGATAAACGAACTGAGCATAGACGATAGAGAAAGAG 603 Qy 541 CATTACAAATTAGAACGATATAGACGCTTAAATGGCTTAACTGGCAACAGAG 600 Db 604 ATGGGGATAGCCCTTCGCTTGGCAAGGCTTGGAACTGTTGTCGCCGGG 663 Qy 601 TGGAGTAATTACCATTAAGTGCCTTGGCGAACGGCTTGGACTTCAGGG 660 Db 664 GATTATCACCCGCCCTCCGGTTGTCAGAGCTTATTGAAAGAACATCTGAGGCC 723 Qy 661 GATTCACCCGCCATGGAGTACASCGCTTCAATTGGAAATATGAGATA 720 Db 724 GC6GCCGATGAAAGGAAGGTGTACASCGCTTCAATTGGAAATATGAGATA 783 Qy 721 ATAGATAGGGAGAGGAGGGATTCAGCCTTTCATCTATCAAATTGGAGGT 780 Db 784 CCAAGGGCGAGTAACTGGAGAGAGAACATTATACCAATAACTCCGTG 843 Qy 781 CCTAAAGTGGAGTAATACAGAGAAGGGTCAATACATATACAGCGTA 840 Db 844 ATGGCACAGAACTGGAAGACTACTATTTCCACCACTATGACATGGCAAAATCAA 903 Qy 841 ATGGTATGAACTGGCTTATGAGTGTAGTAACTGAAATATGAGCT 900 Db 904 GTAAATTATTCATGAGACCTTGAGCTTGGAGGCTTAAGCTTCCGTAASCA 963 Qy 901 GTTCATTATTCATGAAATTAGATACAGATGAGTAAACCTATCGTTCACCG 960 Db 964 GAGAGAGTAT 974 Qy 961 AACAAATAAT 971

RESULT 4 ; Sequence 9817, Application US/10282122A
 US-10-282-122A-9817 ; Publication No. US20040029129A1
 Publication No. US20040029129A1 ; GENERAL INFORMATION:
 - APPLICANT: Wang, Liangsu
 - APPLICANT: Zamudio, Carlos
 - APPLICANT: Malone, Cheryl
 - APPLICANT: Haselbeck, Robert
 - APPLICANT: Ohlsen, Kari
 - APPLICANT: Zyskind, Judith
 - APPLICANT: Trawick, John
 - APPLICANT: Carr, Grant
 - APPLICANT: Yamamoto, Robert
 - APPLICANT: Forbyth, R.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-01-22
 PRIOR APPLICATION NUMBER: 60/205,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 9817
 LENGTH: 969
 TYPE: DNA
 ORGANISM: *Bacillus anthracis*
 US-10-282-112A-9817

Query Match 23.8%; Score 237; DB 7; Length 969;
 Best Local Similarity 55.5%; Pred. No. 2, 5e-60;
 Matches 538; Conservative 0; Mismatches 49; Indels 6; Gaps 4;

```

    Y  4 ATCTGCACAGTCATCTGGAAACTCTGACCGTAAACATGTATTAGCAAGACATG 63
    Y  1 ATCTGTACTTAGTTGAGATTAGACAAAGGTAGCATCTTGTGAGAACGATG 60
    D  64 GATTTCGATTTCAGCTGGGAGAGAGTGATCTCATCCGCCCTACAGCTGAAAC 123
    D  61 GACTTCACATTAGATAGATCAAGAAAGTAAATCATCTCCTGACAACTACAGT 120
    Y  124 AGTGAAGGTGACGAGGGCCATCAGACACAGTACCGGTTATCGSTATGGGAGAA 183
    D  121 AATATAACGGGTAAATGATTAACGAACTAGCTAGGCTCGTCAAATGGTAT 180
    D  184 CTGGAAATATATTGCGGAGGCAATTAGAAACGGTTATCTGTGCGGCCT 243
    D  181 CAAGGAAAGCATTTACCGGAGGAGTAATGAGCGGTTGAGATGTGAAACACT 240
    D  244 TATTTCCCGCTATGGGAGTACGAAAMACGATACGGAGATAACGGTCACATGTC 303
    D  241 TATTTCCAGATTCGCTACTTATAGTCAGATAGTACACACAGAAATTGCT 300
    D  304 CCGCATGAGTTGAGCATGGGTCTGTCACTCTGCAAGCTAAAG 360
    D  301 CCATTGAGTTGAGCTGAGACANTCACTCTGCAAGCCAGTGAAG 361
    D  362 AAAGATGAGTCATTTAACGATGCTGAGAAATAATTAGATCTTGTGCACTCTT 420
    D  361 AATCTGAGATAGATTAACATTACGATTCAGCGGTTAGACTACGCCA 420
    D  421 CGCGTTCAGTGGATATGTCAGCCGGCGAACCTGAGATAGAACAGGCA 480
    D  421 CCACTACATTGGATTAGGGATTAATGGGAGATTGCTGATTCGACAGT 480
    D  481 GACGCCCTCAAGCTGATGAAATCACCTGGTCACTGAGAACAGCCGACTTATA 540
    D  541 TGGCATGTTACCAATCTGGCGAAATATACGAAATGAGCCGAAATTAGAGAGAAA 600
    D  541 TGGATTACAAATTAGACAACTATATAGGCCTTAATCGCAAGCATTGCGCCAA 600
  
```

RESULT 5
 US-10-398-221-766
 Sequence 766, Application US/10398221
 Publication No. US2004018514A1
 GENERAL INFORMATION:
 APPLICANT: KUNST, Frederik
 APPLICANT: GLASER, Philippe
 TITLE OF INVENTION: *Listeria innocua*, genome and applications
 FILE REFERENCE: 344 - US
 CURRENT APPLICATION NUMBER: US10/398,221
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061
 PRIOR FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: FR 00/12 697
 PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025
 SOFTWARE: Patentin version 3.0
 SEQ ID NO: 766
 LENGTH: 990
 TYPE: DNA
 ORGANISM: *Listeria monocytogenes*-EGD
 US-10-398-221-766

Query Match 23.4%; Score 232.6; DB 7; Length 990;
 Best Local Similarity 53.0%; Pred. No. 5, 5e-59;
 Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

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    QY  4 ATCTGCACAGTCATCTGGAAACTCTGACCGTAAACATGTATTAGCAAGACATG 63
    QY  1 ATCTGACAAAGTCGTTGAGATTAGACAACTATGAGAAACATTTATGAGATG 60
    QY  64 GATTTCGATTTCAGCTGGGAGAGAGTGATCTCATCCGCCCTACAGCTGAAAC 123
    QY  61 GATTTCGATTTCAGCTGGGAGAGCCCTACAGACAGTACCGGTTATCGSTATGGGAGAA 183
    QY  124 AGTGAAGGTGACGAGGGCCATCAGACACAGTACCGGTTATCGSTATGGGAGAA 180
    QY  121 TCTCTAAAGCTGGCAATTATGAGATGATGTTGAGGCGAGGAG 180
    QY  184 CTGGAAATATATTGCGGAGGCAATTAGTAAAGGCGTTATCTGTGCGGCCT 243
    QY  181 TTGATAATACHTTTCGAGGGATGAAAGAGGATAAGCTGTCGATCTA 240
  
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QY 244 TATTTCCGGGCTATCGGGAGTAGACGGGAGATAACCGGTACACGTGC 303
Db 241 TATCTTCAGGAAAGCAGTATTGCGCCAGCACAGTGAGAAGAAATCAATTAGT 300
QY 304 CGCGATGAGTTGTCGACATGGGCTCTGCTGTCAGTTGGAGAGTAAGAAA 363
Db 301 CCACAGAACTTTGCTTGGCTGTTAGGAACCTGCGCTTACATGTTAGCAGAACATG 63
QY 364 AGATGAGATTTAAAGTAGTGTAGAGAAGAAATTAGATCTATTGGATACAGTTAACCG 423
Db 361 AAGTTATCGGTTATAACTTGTGTTAGCAACAGTACCGTTACTGGAAACACCA 420
QY 424 CTTCACTGGATATTGTCAGCCGGCGGAACCTGAGGATAGAAACAGGAGAC 483
Db 421 TTACATGGATTTCAGAGAAAGACTGGGGTTGTTACCG 480
QY 484 GGCCCTAAACTCTATGATATCAACCTGGTCTAGACAGAACAGCCGCTTATGG 543
Db 481 TCGCTTGTATAAAGAAACCTGTTAGGAGTATGACAATAACGCCACCATG 540
QY 604 ATGGGGGGATTTAGCCCTTCTGCTTGGSCAAGGTTAGAAGCTGTTGCTCCGGG 663
Db 601 TTGGAGAGATATGCTAAACCATTTCCGAAAGTACAGAACAGAACAAATTACCGT 660
QY 664 GATTTACACCGCTTCCGGTTCTAGGGCTTATGAAAGAACCTCTAGAGCC 723
Db 661 GGTTTACTTCGCCAGAACCTTGTGCGGCACTTGACAGAACAAATTACCGT 720
QY 724 GCGGCGATGAAACGAAAGGTGAAAGCGCTTCAAAATTGGCAAAATATGACGATA 783
Db 721 GCGAAAACCGGAGAAAGTTACAAATGTGGTATGCTGACAGTGTCCGGATT 780
QY 784 CCAAAGGGCCAGTCATAACCGAAAGAGCAAACTCATATGCCAATACTTCGSG 843
Db 781 CGGAAATGGGACGGTTAAAGAAGATGGTGACCTGATTCAACAAATTGTCGATCT 840
QY 844 ATGGCAAGAACCTGGAAACTACTATTCACCTATGACAAATCGGAAATTCAAA 903
Db 841 ATGGTTCCGAAAGCAAGTACTTACCTCATACGAAACACCGAAATCAATG 900
QY 904 GTAAATTATTCATGAAACCTGACTGTGTTGA 938
Db 901 GTTACTTCTGCAAGGAAGTTATGAAATATGAA 935

RESULT 6

US-10-398-221-2682
; Sequence 2682, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221.
; CURRENT FILING DATE: 2003-03-27
; PRIORITY APPLICATION NUMBER: PCT/FR 01/03 061
; PRIORITY FILING DATE: 2001-10-04
; PRIORITY APPLICATION NUMBER: FR 00/12 697
; PRIORITY FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2682
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGDe

US-10-398-221-2682

Query Match 23.4%; Score 232.6; DB 7; Length 990;

Best Local Similarity 53.0%; Pred. No. 5..5e-59; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

QY 4 ATGCGCACAGCTTACATGGAAACTGTGACCTAACATGTTAGCAGAACATG 63
Db 1 ATGCGCACAGCTTACATGGAAACTGTGACCTAACATGTTAGCAGAACATG 60
QY 64 GATTGCAATTGAGCTTGGGGACAGGGATCTCTATCGCGCGTTACAGCTGGAAC 123
Db 61 GATTGCAATTGAGCTTGGGGACAGGGATCTCTATCGCGCGTTACAGCTGGAAC 120
QY 124 ATGAGAGCTGGGGAGGGCCATCAGACAGAACATGCGCTTATCGGTATGGAGAAA 183
Db 121 TCTCTACAGAGGGCCATTATATTAGATATGATATGCTTGGGGAGAGAG 180
QY 184 CTTGGAATAATATTATTCAGGGCTTACAGGATCAGGGAACTAGAAGGGTTATCTGCGCGCT 243
Db 181 TTAGATAATACTATTTCAGGGATGATGAGAAGGGATTAGCTGTTAGCT 240
QY 244 TATTTCCGGCTTGTGCGGAGTAGAAACGATACGGGAGTACCGTTACATGTC 303
Db 241 TATCTTCAAGGAGAGCTTACAGGAGAGCTTACAGGACACAAATTAGCAATTAGCT 300
QY 304 CGCGATGAGTTTGGCTGAGGATGATGAGAAGGGTTATCTGCGCGCT 243
Db 301 CCAGAGAGTTTGGCTGAGGATGATGAGAAGGGTTATCTGCGCGCT 240
QY 364 AAGTTATCGGTTAAACHTGGTGTGATCACAGCTAACGTTACTGATGTTACGTTACG 423
Db 361 AAGTTATCGGTTAAACHTGGTGTGATCACAGCTAACGTTACTGATGTTACG 420
QY 424 CTTCACTGGATTTGACGGTTAGGAGAAGAAATTAGATCTATGGATACAGTTACG 483
Db 421 TTACATGGATTTCAGAGAACAGTACCTCATACGAAACACCGAAATCAATG 480
QY 484 GGCCCTAAACTCTATGACAACTTCACCTGTTGCTGAGCTTATATGG 543
Db 481 TCGCTTGTATAAAGAAACCTGTTGAGGATTTGACAAATGCCACCGATG 540
QY 544 CATGTTACCAATCTGGCAATACTGGAAATGACGAAAGTATAGGAAAG 603
Db 541 CATATGGGAAATTACGAACTACACAGAACATGAGGAAATTCAAA 600
QY 604 ATGGGGGGATTTAGCCCTTCTGTTGGCAAGGCTTGGACTCTGTTCTCCGGG 663
Db 601 TTGGAGAGATATGGTAAACCTTTCGCAAGGATGAGAACGAAATTCACCGT 660
QY 664 GATTTACACCGCTTCCGGTTGGAGCTTGGCTGAGCTTATTTGAAAGAACATCTGGCG 723
Db 661 GGTTTACTTCGCCAGAACCTGTTGCGCAATCTGGAAAGAAATATGAA 720
QY 724 CCGCGGATGAAACGAAAGGTGACCTGGCTTCAATTGGCAATATGACGATA 783
Db 721 CGGAAAGGAAAGAGAGAGACTTACACAGATGTTGGAGATGCTGCGCAT 780
QY 784 CCAAAGGGCCAGCTGAGGAGAGAGAAATTGGCAATATGACGATA 783
Db 781 CGGAAAGGAAAGGAAAGTGGTGGCTTACACAGATGCTGCGCAT 840
QY 844 ATGGCAAGAACCTGGAAACTACTATTCACCTCATACGAAATTCAAA 903
Db 841 ATGGTTCCGAAAGCAAGTACTTACCTCATACGAAACACCGAAATCAATG 900
QY 904 GTAAATTATTCATGAAACCTGACTGTGTTGA 938
Db 901 GTTACTTCTGCAAGGAAGTTATGAAATATGAA 935

RESULT 7

US-10-282-122A-24755
; Sequence 24755, Application US/10282122A
; Publication No. US2004029129A1
; GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forsyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 24755
 LENGTH: 990
 ;
 ; TYPE: DNA
 ; ORGANISM: Listeria monocytogenes
 US-10-282-122A-24755

Query Match Best Local Similarity 23.4%; Score 232.6; DB 7; Length 990; Matches 496; Conservative 0; Pred. No. 5.5e-59; Indels 0; Gaps 0;

OY 4 ATGTGACAGTCCTACATGGAACTGGTACCGTAAGTAGTAACTGGAGAACAGTG 63
 Db 1 ATGTCACAGCTCGTATAGAAACGTTAGTAACTGGAAACATTATTCAAGGAGTG 60
 OY 64 GATTTCGATTCAGCTGGAGAGGATCTCTACCCGGTACACGTGGAC 123
 Db 61 GATTTCGTTTATTGGGGGACCCACAACTAGCCAAAGATTGGATGGAAA 120
 OY 124 AGTGGAGCTGACGGAGGCCCATGAGCAGTACGGCTTTATCGGTTATGGAGAAA 183
 Db 121 TCTTGTACAGACGGTGGCCATTATAATAGATGCTTTGTGGAGGGAGAGAG 180
 OY 184 CTGGAAATTATATTGCGGACGCCATTATGAAAGCGTTACTTGTGGCGCCT 243
 Db 181 TTAGTAAATACATTTCGAGGATGATGAGGAATTGATCAATTGCTA 240
 OY 244 TATTTCCGCGCTATGGGGTACCAAAGATAGGAGAGTACCGTCAATGTC 303
 Db 241 TATTTCCGAGGAGGACTTATGGCCGGCACAGTGGAGGAATTCAATTGCTA 300
 OY 304 CGCGATGAGTTGTCACATGGTCTGCTGCTCTGAGCTTGTGAGAAGCTAAAGAA 363
 Db 301 CCACAGAAATTTCGTTGCGCTTGTAGGACTGGCAAGGATTAAGATGAGGCA 360

QY 364 AAGATTCGATCTTAACGATTTAGGAAATAGATCTTGGATACAGTTACCG 423
 Db 361 AAATTTACGGTTATAACTTGTGATCAACCGTACTGGATCACACCCA 420
 QY 424 CTCACGGATATGGAGAGCCGGCGAAACCTGAGATAGGACAGAGGAG 483
 Db 421 TTACACTGGATTTCAGAGAGAGTGGGGCTTGAGTGGATGAC 480
 QY 484 GCCTCTAACGTTGATGAACTCGTGTGATGAGACAGCCGACTTTATGG 543
 Db 481 TGCCTTGATAAAGAACCTGAGGATGATGACAAATAGCCACGGATCGA 540
 QY 544 CATGTAACAACTGGCAATACAGGAATCAGCCGAGCAATAGAGCAAGAG 603
 Db 541 CATATCAGAATTAGCCTACAGCTACAGGGTTACAGCAACCAATTAGCSCCGGAG 600
 QY 604 ATGGCGGATAGGCCTTCCTCTTGGCCAGGGTTAGGACTCTGGCTGCCGG 663
 Db 601 TTGGAGAGTATGGCTAACATTTCGAGGATGACAGCAAAATTACCGG 660
 QY 664 GATTATCACCGCTTCGGTTGAGCTGTGTTATGAAAGAACATCTAGAGCCG 723
 Db 661 GGTTATCTCCAGAACAGCTTGTGCGTGGGCACTCTGAGAAATTATTA 720
 QY 724 GCGGCCATGAAACGAGGTTAACRGCCCTTTCRAATTGGCAATATGACATA 783
 Db 721 GCGAAAAACGAGAAGAGAGCTATCACAATGTTGGATGCTTGAACAGTGCGGATT 780
 QY 784 CMAAGGCGGAGTGTAAACGGAGAGAACAAATTATACGCAATACTTCGGT 843
 Db 781 CGGAGTGGAGCGGTAATTAGAAAGTGGTGGACCTGTTACACAAATATGGCACT 840
 QY 844 ATGTCACAGAACTGAAACTACTATTCACCACTATGCAATCGCAATTCCAAA 903
 Db 841 ATGTTGCGGAAAGCAACGACTATTCACCTCATACGAAACACCAAACTCAATG 900
 QY 904 GAAATTATTTCATGAGACCTTGACTGTGTTGAA 938
 Db 901 GTTACTTGTGCAAGGAGGTTATGAAATAATGAA 935

RESULT 8
 US-10-429-802-17
 ; Sequence 17, Application US/10429802
 ; Publication No. US20030228285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HUNG, MIEH-CHIE
 ; APPLICANT: WONG, KA YIN
 ; APPLICANT: ZOU, XIU
 TITLE OF INVENTION: BIPARTITE T-CELL FACTOR (TCF) - RESPONSIVE PROMOTER
 FILE REFERENCE: US/USC:752US
 CURRENT APPLICATION NUMBER: US/10/429,802
 CURRENT FILING DATE: 2003-05-05
 PRIOR APPLICATION NUMBER: 60/377,672
 PRIOR FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: Patentin Ver. 2.1
 SEQ ID NO: 17
 LENGTH: 1616
 ;
 ; TYPE: DNA
 ; ORGANISM: Bacillus sphaericus
 US-10-429-802-17

Query Match Best Local Similarity 17.4%; Score 173.8; DB 6; Length 1616; Matches 495; Conservative 49.8%; Pred. No. 4.1e-41; Indels 6; Gaps 2;

OY 7 TGCCTCAACTCTACATGGAAACTGCTACCGTAACAGTGTGAGGATGCTA 66
 Db 335 TGCAGTAGCTTATCAATCTGATAACAGATGATAAGTTATCGCTGCACTGGAT 394
 QY 67 TTGCATTCAGTGGGACAGGGTATTCTATGGCGGTTACGTCGAAACAGT 126

Db	3.95	TTCAGATGGACCAAGATAGTAAAGCTATTGTCACCGTAATTACGGATTCTGATT	454
Qy	1.27	GAAAGCTGACCGAA - -GGGCCCATAGACAGTAGCGGTITATCGSTATGGGAGA -	181
Db	4.55	T TAGAAAGAAAATGTAGTCATTACAACTCATATGCTTTGGAATGGAACT	514
Qy	1.82	-AAGTTGAAATATTTATTGCGCAGGGCTTATGAAAGGGTTATCTGIGCGGG	240
Db	5.15	GACATTAACATCACCGTCTCTATAGTGCGGTAAGAAAGGGATAATGGCGGAT	574
Qy	2.41	CTTATTTCCGGGTATGGGAGATCGAAAAAACATACGGAGATACCGTTACATT	300
Db	5.75	CTTACTATGCTACATTGCGACTTATGCTGAGCACTAAAGGCACACAGGGATC	634
Qy	3.01	GTCCGGCAGAGTTGTGACATGCGTGTGCACTGTCGTTGGAGACCTAAA	360

; TITLE OF INVENTION: TARGETING PROTEINS TO DELIVER THERAPEUTIC OR DIAGNOSTIC
; TITLE OF INVENTION: REAGENTS
FILE REFERENCE: USPC:7970US
CURRENT APPLICATION NUMBER: US/10/430,503
CURRENT FILING DATE: 2003-05-05
PRIOR APPLICATION NUMBER: 60/383,063
PRIOR FILING DATE: 2002-05-06
NUMBER OF SEQ ID NOS: 42
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO: 8
LENGTH: 1616
TYPE: DNA
ORGANISM: *Bacillus sphaericus*
US-10-430-503-B

Db	635	AATCCCGCTATGTAATTCTCAAGTTAGGAATGTGTAACGTGATGATTTATT	694
Qy	361	GAAAGATTCGATCCTTAAAGATGTTGAGAAAATTAGCTCTTGGATACASITTA	420
Db	695	GAAATTACTCTTATACATTTGAACTGAGGCAATAATACCTTG3CACCC	754
Qy	421	CCCTCACTGGATTTGTGAGACGGACGGGCCAACCTGACCTAGAACAGCA	480
Db	755	CCACTCTACTATACATTTACAGATGCTTCTGGTGTATCGATGTTATTGAAACGATAA	814
Qy	481	GACGGCTCAAGTCTATGTAATACCTGGTGTATGAGAACAGCCGACTTTATA	540
Db	815	ACAGGATACCATTCATCGAAAGATGGCGTATGAGAACAGAACAGACATGAA	874
Qy	541	TSGCATGTAACCAATCTGGCAATATACGGATTCAGACCGAACATTRGAGACAA	600
Db	875	TGCATCGACAAATTAAAGACTTACATGTTGCTCACACAAATCCGCCAACATA	934
Qy	601	GAGATGGGGATAGCCCTTCGCTTTGGCCAGGCTTAGGACTGTGTTGGCG	660
Db	935	ATGATGGGAGACTTGTGATTCACACCGTTGGCAGGGCTTAGGATTTACCA	994
Qy	661	GGGGATTAACACGGCTTCCGTTGGTCAAGCTGGTTATTGAAAGACATCTAGAG	720
Db	995	GGTGTATTACGGCTCAGCACGTTCTCGGGTACATGCAACTGAAATATCTGAA	1054
Qy	721	CGGGCGCGATGAAACGAAAGGTCTAAGCCCTTCAATTGGCAATGAC	780
Db	1055	AAAGCCAAAATGAAACGAGGCGCTAACACTTGTCAATTCTGTAAT	1114
Qy	781	ATACCAAGGGCGGAGGATAACGGAAAGAGGAAATCTATACGGCATATCTCC	840
Db	1115	ATCCCCAAAGGTCTTGTGATGAAATGGGGAAACGGATTAACCTCTATCTCA	1174
Qy	841	GTGATGTCACACAAACTGAAACTRACTATTTCCACACTATGCAATGGCAAATCCAA	900
Db	1175	GCTATGTCACACAAACTTAACTTAACTGATGATGATGCTGAAATTCTCA	1234
Qy	901	AAAGTAATTATTTCTGAAAGACCTGGTACTGTTGGCTTAAGTGTTCGCTAA	960
Db	1235	GCGTGTTCCTTATGCTGAAATTAAATGTCAGAATTAACTTACATTGAGGGAT	1294
Qy	961	GCAGAGAGAGATTCTGAGCTTAAAGGA	993
Db	1295	CGTAACAAAGATTTAGCAATTAACTGAGTA	1327

US-10-430-503-8
; Sequence 8, Application US/0430033
; Publication No. US20040056441
GENERAL INFORMATION:
; APPLICANT: HUNG, MIEU CHIE
; APPLICANT: LAN, KENG-LI
; APPLICANT: OU-YANG, FU
; APPLICANT: LIU, JAH-CHING
; APPLICANT: LAN, KENG-HSIN

RESULT 10
US-10-282-122A-34300
; Sequence 34300, Application US/10282122A
; GENERAL INFORMATION:
; APPLICANT: Wang, Liangsu
; APPLICANT: Zamudio, Carlos
; APPLICANT: Malone, Cherry
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari
; APPLICANT: Zyskind, Judith
; APPLICANT: Wall, Daniel
; APPLICANT: Trawick, John
; APPLICANT: Carr, Grant
; APPLICANT: Yamamoto, Robert
; APPLICANT: Forbyth, R.
; XU, H.
; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
; FILE REFERENCE: ELITRA_034A
; CURRENT APPLICATION NUMBER: US/10/282,122A
; CURRENT FILING DATE: 2003-02-20
; PRIOR APPLICATION NUMBER: 60/191,078
; PRIOR FILING DATE: 2000-03-21
; PRIOR APPLICATION NUMBER: 60/206,848
; PRIOR FILING DATE: 2000-05-23
; PRIOR APPLICATION NUMBER: 60/207,727
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 60/230,335
; PRIOR FILING DATE: 2000-09-05
; PRIOR APPLICATION NUMBER: 60/230,347
; PRIOR FILING DATE: 2000-09-09
; PRIOR APPLICATION NUMBER: 60/242,578
; PRIOR FILING DATE: 2000-10-23
; PRIOR APPLICATION NUMBER: 60/253,625
; PRIOR FILING DATE: 2000-11-27
; PRIOR APPLICATION NUMBER: 60/257,931
; PRIOR FILING DATE: 2000-12-22
; PRIOR APPLICATION NUMBER: 60/267,636
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: 60/269,308
; PRIOR FILING DATE: 2001-02-16
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 78614
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 34300
; LENGTH: 978
; TYPE: DNA
; ORGANISM: Staphylococcus epidermidis
; US-10-282-122A-34300

Query Match 16.1%; Score 160.2; DB 7; Length 978;
Best local Similarity 49.9%; Pred. No. 4e-37;
Matches 458; Conservative 0; Mismatches 453; Indels 6; Gaps 2;

QY 901 AAAGTAATTATTATTCATGAGACACTTGACTGTGGAGCTAAAGGTTTCGGCTAA 900
Db 1235 GCGGTTCTTAATGCTGAATAATTAAATAGTCAGATTAACTTGTGGGGAT 1294
QY 961 GCAGAGAGAGGATTCATGACTTAATTAGGA 993
Db 1295 CGTAAACAGAGATTAAGCAATTACAGTA 1327

RESULT 11
US-10-724-972A-1455
; Sequence 1455, Application US/10724972A
; GENERAL INFORMATION:
; APPLICANT: Doutette-Stamm, Lynn
; APPLICANT: Bush, David
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
; TITLE OF INVENTION: EPIDERMODIS FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: PAPHO-16
; CURRENT APPLICATION NUMBER: US/10/724,972A
; CURRENT FILING DATE: 2003-12-01

QY 64 GATTTCATTTCAGCTGGAGAGGGATTCCTCATCGCGCCTACGCTGAAAC 123
Db 61 GACTTCATTTGATTAACTGATCCACCATGTTCCAGTCATATCACCAA 120
QY 124 AGTGAACTGACGGAAAGGCCATCAGAACAGTAGCGTTATCGGATGGGAGAAA 183
Db 121 TTGATCTAGATCA--GACATGCCTCTGATATGGTTTGGTGAAACAATTAAA 177
QY 184 CTGGAAATATATTGCCCACGSCATTATGAAAGCGGTATCTTGCGCGCCT 243
Db 178 GTAGGAGTTATAGATTTGGATGGATAACGAAAGGTATGGTTCAGCTGACCAT 237
QY 244 TATTTCGGCTATCGGAGTACGAAAAGATACGGAGATACGGTCACATGTC 303
Db 298 CCTGAGGGTTATTGTTGGTTTAATAAGATTTAGGAAATTAACACAA 357
QY 364 AAGATTCATCTTAACGATTCAGGAAATTAAGATCTATGGGATACCTTACCG 423
Db 358 AAGGTTAGAGATCATATATGAGTAACTTGAAAGAAATCAACTTGAAATCTCC 417
QY 424 CTRGACTGGATTGTCAGACGGGACGGAACTGAGATAGACAGGAGGAC 483
Db 418 TTACATTTCATGTCATGAAACAGACATACCTGATAGACCTCACATGGC 477
QY 484 GGCTCAAGCTATGATGACTGACTGGTCTGAGACAGCCGACTTATTTGG 543
Db 478 TTATTAACTGTTAAGTAATTATGTCATACCTAACAAATGCGCTTAATTAGTGG 537
QY 544 CAGTAAACAACTGCGCAATAAACGGAACTGAGCAATAGAGCAGGAG 603
Db 538 CATCTACTAACTTAAGAAATTATGTTAACACACAGAAATCACCATCAAA 597
QY 604 ATCGGCCGATAGCCCTTCCTTGGCCAGGGCTTAGGAACTGTGGTCGCCCG 663
Db 598 ATAGTAAAGTGTAGTAATGAGTCATGGGTTGAAACGAGGAAATGGCTTACCGGGT 657
QY 664 GATTATCACCCCTTCGGGTTGAGAGCTTATTGAAAGAACATCTGAGCCG 723
Db 658 GGTTATCTTCACAGAGCTTATGGGACATATTAGACCAACTACCGGT 717
QY 724 GCGGCCGATGAAAGGAGGTTACGCCGTTCAATTGGCAATGACCA 783
Db 718 TCCATATGAGATGAATTAACTTATGTTAACTTCTAGATCAGTCAGPAC 777
QY 784 CCAGAGGCGCAGTGTACGGAGAGAGGAAATTATAGCTATACTTCGGT 843
Db 778 CCTCAAGGTGCGATT--CGATGCCATATAATGATACAGAATATCATGTTG 834
QY 844 ATCTGCACGAAACTGAAACTACTATTCACCATGACATGGAAATCCAAA 903
Db 835 ATGGAAAGTAAAGAAGAGCTTATTAAGCCATACCTAGATCAAAATTCAA 894
QY 904 GAAATTAACTCATGA 920
Db 895 ATAAATTAACTGAGA 911

PRIOR APPLICATION NUMBER: 09/450, 965
PRIOR FILING DATE: 1999-11-29
PRIOR APPLICATION NUMBER: 09/134, 001
PRIOR FILING DATE: 1999-08-13
PRIOR APPLICATION NUMBER: 60/064, 964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: 60/055, 779
NUMBER OF SEQ ID NOS: 7544
SEQ ID NO: 1455
LENGTH: 996
TYPE: DNA
ORGANISM: *S. epidermidis*
US-10-724-972A-1455

Query Match 16.0%; Score 159; DB 7; Length 996;
Best Local Similarity 49.8%; Pred. No. 9.2e-37;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 2 ATATGTCGCAAGCTTACATGGAAACTGTGCGTAAACAGTTAGCAAGAACRA 61
Db 14 ATATGTCGACTGCCATTATATAACAAACAGTACATTAGCTAGAACACA 73
QY 62 TCTGATTGCAATTCTAGCTGGGACAGGGTATTCTATCCGGCCTACAGCTGGA 121
Db 74 TCGACTTGCATTGTAATTAATGCTATGCCAACATGTCAGGCCATTACTACC 133
QY 122 ACAGTGGAGCTGAGGAAGGGCCATCGACACAGTAGCGCTTATCGSTATGGAGA 181
Db 134 ATTGATCTAGATTAGACATGGCTT--GAAATGTTTGTGGAACAAATTAA 190
QY 182 AACTTGGAAATAATATATTGCGAGCGCATTTATGAAAGCGTTATCTGGCGGCC 241
Db 191 AATGTTAGACAGTTATAGATTTGGTGATGGTGTGTTAGCTTACGAAACC 250
QY 242 TTATTTCCGGCTATCGGGGATCGAAAAAACGATAGGGAGAACCGTCAATG 301
Db 251 ATTACTTCACTGGTGAATACCTAACATTAACGTTAGTGTATTACTAG 310
QY 302 TCCCGCATGAGTTGTCATGGGTGCTGTCAGTCTGTCAGTTGGAGCTGAAAG 361
Db 311 CACCTGAGGAGTTATGTTGGGTTAGTTTAAATAAAGTATAGCGGATTAAAC 370
QY 362 AAAAGATTCGATTTACGTTGAGGAAAATAGATCTTGTGATACGTTAC 421
Db 371 AAAAGCTTAAGAAATACATATTATGATGAAAAAATACGACTTGTGATACGTTAC 430
QY 422 CGCTTCACTGGATATGTCAGACGGGAGGGCGAACCTGAGGATGAAACAGASCAG 481
Db 431 CTTTACATTCTGGTCACTGATGAAACAGGACATACGGCTACAGCTCACATG 490
QY 482 ACGGCCCTCAAGTCTGATATACTACCTGGTGTGTCAGACAGGCCGACTTAT 541
Db 491 GCTTATAATAGATAAGATAATATGTCATACCTTACAAATGAACTTAAATTGATT 550
QY 542 GGCACTTACCAATCTGCAGCAATATACAGGATCAGCCGAACTTGGCTCGGG 601
Db 551 GGCATCTATCTGACTTAAAGATAATACCTCTTAAAGCCACAGAACTCAACAAAT 610
QY 602 AGATGGCGGGAATTAGCCCTTCTGCTTGGCAAAGCTTAACTGGAACTGGTCTCGG 661
Db 611 TAATAGTAAAGTGTCAAGTAACTGGGTGTGAGCAGAACAAATGGCTACGG 670
QY 662 GGGATATACACCGCCCTCCGGTTCTGAGCTTATTGAGAACTCTGAGC 721
Db 671 GTGGTATACGTCACAGATCTTATACGGCTACATTTAAAGCTACGCT 730
QY 722 CGCGCGCCGATGAAAGCAAGGTGACAGCGCTTCAATTGGCAATATGCGA 781
Db 731 GTTCCCATAATGAAAGTGAATTTAGTGTGTTAAGTCAGTCAGTCAGTA 790
QY 782 TACCAAGGGCACTGATAAGGAAAGAGCAAGTACATATGGCAATACTTCG 841

RESULT 12
US-10-282-122A-7960
Sequence 7960, Application US/10282122A
Publication No. US200400029129A1
GENERAL INFORMATION:
APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haelbeck, Robert
APPLICANT: Ohlisen, Karl
APPLICANT: Zukind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Travick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
FILE REFERENCE: ELTRNA_04A
CURRENT APPLICATION NUMBER: US10/282,122A
CURRENT FILING DATE: 2003-02-20
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: 60/230,335
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/230,347
PRIOR FILING DATE: 2000-09-09
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR APPLICATION NUMBER: 60/253,625
PRIOR FILING DATE: 2000-11-27
PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/267,636
PRIOR FILING DATE: 2001-02-09
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR FILING DATE: 2001-02-16
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 78614
SOFTWARE: PatentIn version 3.1
SEQ ID NO: 7960
LENGTH: 993
TYPE: DNA
ORGANISM: *Staphylococcus aureus*
US-10-282-122A-7960

Query Match 14.7%; Score 146; DB 7; Length 993;
Best Local Similarity 47.5%; Pred. No. 7.7e-33;
Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

QY 4 ATGTGCAAGGCTTACATGGAAACTGTGCGCTAACATGTTAGCAAGAACATG 63
Db 1 ATGTGCAAGGCTTACATGGAAACTGTGCGCTAACATGTTAGCAAGAACATG 60
QY 64 GATTTGCAATTCTGGGAGAGGGTGTCTCTATGGCGCGTACAGCTGGAC 123
Db 61 GATTTGCAATTCTGGGAGAGGGTGTCTCTATGGCGCGTACAGCTGGAC 120

Qy 124 ACTGGAAGCTGACGGAAAGGCCCATCACACACAGTACCGTTATCGGTTATCGGAA 183
Db 121 TGTGCACT--GGCAGACAGCCAAACGATATGGCTTATGGTACAGAACGAT 177
Qy 184 CTGGAAATATTATTGCGCACGCATTATGAAAGCGGTTATCTGGCGGCTT 243
Db 178 ATGGAGGTTPATTATGGTATGGTACATGGCTTATTCGACAA 237
Qy 244 TATTCGGCTATGGGAGACGAAACCATACGGAGATCGGTACATGGC 303
Db 238 TATTCGGGTTATGTCATGGTACAGTGGGATACACAAAGCGACGGAT 297
Qy 304 CGCGATGAGTGTGACATGGGCTGTCAGTCGTCAGTCGTTGGAGAGCTAAGAA 363
Db 298 CAAATGAAATGTCATGGTACATGGTACAGTGGGATACACAAAGCGACGGAT 357
Qy 364 AGAGATGATCTTAAGATGAGBAAAATTACATCTATGGTACAGTGTACCG 423
Db 358 CAAGCATCCAAATACATGTGTCAGCTGCTATATTAAATGACATCGGTGAACTTCGGCA 417
Qy 424 CTCACTGGATATGTCGAGCCGACGGCCGAAACCTGACGAGACAGAC 483
Db 418 TTGCAATTATGTCGATGACTTCGATGAACTGGAACCTGCACTGAGGT 477
Qy 484 GGCCTCAAAGCTATGATAATCACCTGGTGTACAGGACAGAGAC 543
Db 478 GAAGGGTTATAAGATACACCTATGGTGTACACATCCGAGCTAGATGG 537
Qy 544 CATGAACTGACAACTGACGAAATACAGGATCAGACGGAACTTAGAGACAGAG 603
Db 538 CATTATGTTAAGACATATCATATTCTCTTATCCGAAACGAAAGTA 597
Qy 604 ATGGCGGATAGCCCTTCGTTTGCGCAAGCTTAGAAGCTGGTGGCGGG 663
Db 598 TTGGAAGSTGTACGATGAACTTGGCAATGAGACGGTCAATTGGCGGT 657

Query Match 14.7%; Score 146; DB 2; Length 11466;
Best Local Similarity 47.5%; Pred. No. 2. 9e-32; Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;
Matches 468; Conservatve 0; Mismatches 515; Indels 3; Gaps 1;
Qy 664 GATGATACCGCCTCCGGTTGTCAGCTGTTATTGAAAGAACATCTAGAGCC 723
Db 658 GGTTTACTTCACTGCGCTTGTGAGAATGCAATTGAAAGAACATGCTCAA 717
Qy 724 GCGCCGATGAAAGGAAGGGTGTACACCGCTTTCAAATTGGCAATATGACGATA 783
Db 718 AACATGATAAGAATGGATTATGATGCAATTATGAGTCGGTAATA 777
Qy 784 CCAAGGCGCACTGATAACGGAGAACGAAATTCTATTATGCAATATCTGGT 843
Db 778 CCCTTGTGATGTCGCGCTGATGTCGACATCTATGATGTCGACCGATA 837
Qy 844 ATGTGCAACGAACTGGAACTTCCACCATGACATGGCAATCCAAA 903
Db 838 ATAATTTTACATGAGACGTTATATTAATGATGCGACATGAGTAGCA 897
Qy 904 GTAAATTATTCATGAACTTGACTCTTGGGCTTAAGTGTTCGCTTAAGCA 963
Db 898 TTAGCTCACAGATGATTATAGAAAGATAGCGATTAGCTGAGAG 957
Qy 954 GAAGAGAGATTCTGAGCTTAATA 989
Db 958 CATTACATTTAGACAGTGA 983

RESULT 13
US-08-781-986A-44/c
Sequence 444, Application US/08781986A
Publication No. US20030054436A1
GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255
CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville

STATE: Maryland
COUNTRY: USA
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 444:
SEQUENCE CHARACTERISTICS:
LENGTH: 11466 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

US-08-781-986A-444

Query Match 14.7%; Score 146; DB 2; Length 11466;
Best Local Similarity 47.5%; Pred. No. 2. 9e-32; Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;
Matches 468; Conservatve 0; Mismatches 515; Indels 3; Gaps 1;
Qy 4 ATGTGCAAGCTTACATGAACTTGGAACTGCTGACCGTAACTGAGACATG 63
Db 3688 ATGTGCAAGCTTACATGAACTTGGAACTGCTGACCGTAACTGAGACATG 3629
Qy 64 GATTTCATTCAGCTGGGGACAGAGGTTGATCTCTATCCGGCCCTAACGTGGAC 123
Db 3628 GATTAATTATCCATTAGATGTTGGCTCCAGGAGTGGCTTAAAGATGTTGGAA 3569
Qy 124 ACTGGAAGCTGACGGAAAGGCCATCACACAGTACGGTTATCGGTTATCGGAA 183
Db 3568 TCTGTCAGT--GGCAGACAGCCAAACGCAATATGCTTATGGCAGACAGT 3512
Qy 184 CTGGAAATATTATGGCAACGGAAATAGAAAGGGTTATCTGGGGCTT 243
Db 3511 ATGAAAGCTTATGGTGTGATGGTTATGAAAGATGCGTSCATTCAACAA 3452
Qy 244 TATTCGGCTATGGGAGACGAAACGATACGGAAATACGGAAATACGGTACATGTC 303
Db 3451 TATTCGGCTATGGTGTGATGGTCAACACAAAGCGACGGGATGATATACG 3392
Qy 304 CGCGATGAGTGTGAGATGGGCTGTCAGTCGTCAGTCTTGGAGACCTAAGAA 363
Db 3391 CAAATGAAATGTCATGGTTCGGATATACACAAAGGATGAGATGAA 3332
Qy 364 AGAGTCACTTAAAGATGAGGAAATAGCTTGGTACAGTGTACGGT 423
Db 3331 CAAGCATCCAAATACATGTTGAGCTTATTAATGACATCGGTGAACTTCGGCA 3272
Qy 424 CTCACTGGATATGTCGACCGACGGCCGAAACCTGACGATAGACAGAC 483
Db 3271 TTGCAATTATGTCGATGTTGGCTGACATGAGTGGCTTATTAAGAGGT 3212
Qy 484 GGCCTCAAAGCTATGATAACCTGGTGTACAGGAAACGCCCCGACTTATGG 543
Db 3211 GAAGGGTTATAAGATPAATCTTATGGTGTACACATCGCACTTAATGG 3152
Qy 544 CATTACCAACTGCGCAATACAGGAAATAGCGAAACGAGCAATAGAGACAGAG 603
Db 3151 CATTATGTTAAGACAAATATCAATATCTCTTATCCAGCAACAGCAATTAA 3092

QY 604 ATGGGGGATTAAGCCCTTCGCCTTGCCAAAGCTTACGAACTGTGGTCTGCCGGGG 663

Db 3091 TTGGAAAGGTGTAACGATGAACTTCTAGGATGAGCAGTACATTGATGCCAGGT 3012

QY 664 GATTTACCCGCTCCCGTTGAGCTTATTTGAAGAACATCTAGAGCG 723

Db 3031 GGATTTACTTCACCTGAGGCTTGTGAGAATGGATTATGAAACATCTCGA 2972

QY 724 GCGGCCGATGAAACGAAAGGTAAACAGCGCTTTCATAATTGCAATATGAGCAGCG 783

Db 2971 AACATGATGAAACGAAATGATGTTATGATGCTTATTATGATGGGGAAATATA 2912

QY 784 CCAAAGGGCCAGTATAAGGAAAGAGGAATTCATTAACGAAATACTCCGG 843

Db 2911 CCGATGGAATGTTAGTCGGCATGATGCGACATCATATGATGATCACCGTA 2852

QY 844 ATGCGCAACGAACTGGAACACTACTATTCACCTACATACATACATGGAAATCAA 903

Db 2851 ATAATTTAACATACAGAAAGTTATATTAAGTATGGAGCTTAAGGAAATGAG 2792

QY 904 GTAATTTATTCATGAAACCTTCACCTTGAGCTTAAGGCTTAAGTGGAAATGAG 963

Db 2791 TAAAGCTTACAGTATGTTATTAATGAAAGTATGAGTTTACGTTGAGAG 2732

QY 964 GAAGAGGAGTATCAGTAAATA 919

Db 2731 CATACTACTATTAGAAAGTGAATCA 2706

RESULT 14

US-10-329-624-44/c

Publication 444, Application US/10329624

Publication No. US20040043037A1

GENERAL INFORMATION:

APPLICANT: Charles Kunisch

G.I.H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 5.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-DEC-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: P248P1D1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 319-8439

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 11466 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

US-10-329-624-444

Query Match 4 ATGCGCACAGTCATCATGGAAACTGCTGACCGAAACATGTTACCAAGAACATG 63

Best Local Similarity 47.5%; Pred. No. 2.9e-32; Length 11466; Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

Db 3688 ATGTCACAGGATTACATACAACTTTAAATTATCATGACTCTTCTTGACGCCAGATG 3629

QY 64 GATTTGCAATTGAGCTGGGGCTAGGAGCTGATCTTACCGGCTAGGCTAGAATTTGGAAAC 123

Db 3628 GATTTGATTCAGTATGATGTTGCGAGCTGAGCTGAGCTGAGCTGAGCTGAG 3569

QY 124 ATGCGAGCTGACGAGGGCCATAGACAGACAGTACCGGTTAGCTATGGTATGGAA 183

Db 3568 TCTTGACTT-GGACGACAGGCCAACGCAATAGCTTATGGCTAGGAAATATGGAA 3512

QY 184 CTGGAAATATTTATGCGACGCTTAATGAGCGTTTATCTTGCTGGCGCT 243

Db 3511 ATGGAAGGTTTATTATGGTGTGTTAATGACATGGCTTGCATTACACAA 3452

QY 244 TATTTCGGCTATGCCAGGAGGAGAAACGATACCGGAGATACGGTTACATGTC 303

Db 3451 TATTTCGGCTATGCCAGGAGGAGAAACGATACCGGAGATACGGTTACATGTC 3392

QY 304 CCGCATGAGTTGAGCTGGGGCTGCTGAGTCATGTCTGTAGTCAGTCTTGAGACGTAAGA 363

Db 3391 CAAATGAAATTGAGCTTGGGGATGAGCTTAACTACACAGCTTGGGGATGAGATGAA 3332

QY 364 AACATGCACTTAACTGGAGAAAAATTAGATCTATGGATACTGGTTACAGTTTACCG 423

Db 3331 CAAGCATCCAAATACTGGTTAGCTGTATTTAAATGACATCGGGAGTTCGCGCA 3272

QY 424 CTTCAGGATATGTCGACCGAGGGGGCGAACTGACGATAGCTGAGTGGAGAG 483

Db 3271 TGGCATATCAGTTGCGACCGAGGGGGCGAACTGACGATAGCTGAGTGGAGGGT 3212

QY 484 GCCTCAAGTCTATGATAATCAGTCACCTGCTGTCATGGAGACAGCCCCGACTTTATGG 543

Db 3211 GAAGGGTTATAAAGATACTCTATGGTGTCTAACATCCAGCTAAATGG 3152

QY 544 CATGAACTCTGCGCAATACTGGGAACTGAGCGAAATTTAGAGAGCAAGAG 603

Db 3151 CATTATGAAATTAGACAAATACTAAATTTCTCTTACGCAACAGCAATTAA 3092

QY 604 ATGGGGGATTAAGCCCTTCGCCTTGCCAAAGCTTACGAACTGTGGTCTGCCGGGG 663

Db 3091 TTGGAAAGGTGAACTGAGCTTACGGCTTGTGAGCTGAGCTGAGCTGAGCTGAGGT 3032

QY 664 GATTTACCCGCTTCCCGTTGAGCTGAGGTGTTATTTGAAGAACATCTAGGCCG 723

Db 3031 GGATTTACTTCACCTGAGCGTTTGTGAGAATGGCTTATGAAACAACTGCTCAA 2972

QY 724 GCGGCCGATGAAACGAAAGGTAAACGCCCTTCAAAATTGSCAAATATGACGATA 783

Db 2971 AACATGATGAAACGAAATGGTTATGATGCTTATTATGATGCTGAGCTAATGAG 2912

QY 784 CCAAAGGGGAGGTGAAACCGGAACGAACTTCAATTTGSCAAATATGACGATA 843

Db 2911 CGATGAAAGGTGAGCTCCGATGTCGACAACTACATGAGTGTGAGCTGAGCTA 2852

QY 844 ATGCGAGGAAACTGAAACTACTTCTACCACTGAGCAATGGCAATTCACAA 903

Db 2851 ATAATTTAACATACAGAAACCTTATTAATGAGTATGGAGCTGAGTGTGAG 2792

QY 904 GTAATTTATTCATGAGACCTTCACCTGAGCTGTTGGAGCCCTAAAGTGTTCGCTAAAGCA 963

Db 2791 TAAGCTTCACAGATGATTAAATGAAAGATATCGCGATTAGCCCTGGAGAG 2732
 Qy 964 GAAGAGAGTATTCTATGAGCTTAATAA 989
 Db 2731 CATACTACTTTAGAAGTGAATCA 2706

RESULT 15
 US-09-815-242-8383
 ; Sequence 8383, Application US/09815242
 ; GENERAL INFORMATION:
 ; Patent No. US20020061569A1
 ; APPLICANT: Hasebeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Travick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard

TITLE OF INVENTION: Identification of Essential Genes in Prokaryotes

FILE REFERENCE: ELITA_01A

CURRENT APPLICATION NUMBER: US/09/815,242

CURRENT FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/223,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/259,308

PRIOR FILING DATE: 2001-02-16

NUMBER OF SEQ ID NOS: 1410

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO: 8383

LENGTH: 1002

TYPE: DNA

ORGANISM: Staphylococcus aureus

FEATURE: CDS

NAME/KEY: CDS

LOCATION: (1) .. (1002)

; US-09-815-242-8383.

Query Match 14.3%; Score 142.8; DB 3; Length 1002;
 Best Local Similarity 47.3%; Pred. No. 7.2e-32;
 Matches 466; Conservative 0; Mismatches 517; Indels 3; Gaps 1;

Qy 4 ATGTGCACAAGCTTACATGGAAACTGCTGACGCCAACATGTTAGCAGAACATG 63
 Db 10 ATGTGCACAAGGTTACATGGAAACTTAAATCAAGCTCTTGACGACGATG 69

Qy 64 GATTGCGATTCAGCTGGGACAGGGATCTATCGCGCCGTTACGCTGGAAC 123
 Db 70 GATTGCGATTCAGCTGGGACAGGGATCTATCGCGCCGTTACGCTGGAAC 129

Qy 124 AGTGAAGCTGACGGACGGCCATACAGCTAGCTGGGTTATCGTAGGGAA 183

Db 130 TCTCGCACT--GGCACGAAGGCCAACGCCATATGCGTTATGGACAGATG 186

Qy 184 CTGGAAATAATTATGGCCAGGGCATTAAGAAGGGTTATCTGGCTAAGGAA 243

Db 187 ATGGAAAGCTTATTATGGCTATGAGCTTAAATGAGCTGGCTAACACAA 246

Qy 244 TATTTCGGGCTATGGCGAGTACGGAAAATGATACGGAGAGATCCGTTACATGTC 303

Db 247 TATTCCGGGTTATGTCATAGGTCACACACAGGGATGCGATGAAATACG 306
 Qy 304 CCCCATGAGTTGTCAGATGGGGCTTCAGTGTGTCAGTCAGGAGCGTAAGAA 363
 Db 307 CAAAATGAAATTGCACTGAGTGGATTTCGGATATACACAGCATGAGATGAA 366

Db 364 AAGATTCGATCTTAACTGATGGAGAAAATTACATCTATGGATACAGTTACG 423
 Qy 367 CAGGCATCCCAAATACATGTTGAGCTGTTAAATGATATCAGGAGTCCCA 426

Db 424 CTTCAGCTGGATATGTCAGACGGACGGGCGAAACCTGACGATGAGCAAGGGAC 483
 Qy 427 TTGCATATCATGTTCCGATGCACTGACATCAGCTGGAGTTTAAAGAGGG 486

Db 484 GGCTCCTAAGTCATGATGATCAGCTGGCTGAGCTGAGACAGGCCGACTTATGG 543
 Qy 487 GAATGTTATATAAAGATAACCTTATGGTGTCTTAACTACATCCAGACTTGTGG 546

Db 544 CAGTAACTTCTGGCCAAATACAGGAATCTGAGGAACCTGAGCTGGTCTCCGGG 603
 Qy 547 CATTATGTTAACTTAAAGACAATATATCATTCTCTTATCCAGCACGAA 606

Db 604 ATGGCGGAAATTAGCCCTTCGCTTGGCCAAAGCTTAACTGGAGACTGTTGCTCCGGG 663
 Qy 607 TTGGAGGTGAACGATGAACTTACAGCTGGAACTGAACTTGGATGCCAGT 666

Db 664 GATTATCACCGCTTCCGGTTGTCAGGCTTATTGAAAGAACATCTGAGCG 723
 Qy 667 GGATTTACTCAACTGAGGGCTTGTGAGATGCTGCAATTATGAAAGCAACATGCTCA 726

Db 724 GCGCCGTTGAAACGAAAGGTGTACAGCCGCTTCAATTGGCAATATGAGGATA 783
 Qy 727 AACATGATAAGAAATTGATGTTATGATGCAATTATTAGTCGGTAATAATA 786

Db 784 CCAAGGGCCAGTGTAAAGGAAGAGACGAAATTATTGCAATTATGCTCAATTACCTCCGG 843
 Qy 787 CCGATGGGATTGTACGTCGCTGATGCTGACATCACTATGACGACCGTA 846

Db 844 ATGTGCACAAACTGGAACACTACTATTCACCACTATGACAACTGGCAATTCAA 903
 Qy 847 ATAATTTAACTACAGAAACGTTATATAAGTATGGACGACATGAAATAGCA 906

Db 904 GTAAATTATTCATGAAACCTGACTCTTGGCAAGCTTCCGCTAAAGCA 963
 Qy 907 TTAAAGCTCACAGTGTATTAAATGAAAGATATGACGATTITTAAGCTGAGA 966

Db 964 GAAGAGAGTATTCTGAGCTTAATAA 992
 Qy 967 CATATCACTTAAAGTGAATCA 992

Search completed: March 18, 2006, 13:28:30
 Job time : 998 sec

GenCore version 5.1.7
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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:54:08 ; Search time 452 Seconds

(without alignments) 5138.006 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 996

Sequence: 1 catatgtgcacaaggcttac.....atgagtttaatggatcc 996

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 10%

Listing first 45 summaries

Database : Published Applications_NA_New:*

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2: /cgn2_6/prodata/1/pubpna/us05_NEW_PUB.seq: *
3: /cgn2_6/prodata/1/pubpna/us07_NEW_PUB.seq: *
4: /cgn2_6/prodata/1/pubpna/pctc_NEW_PUB.seq: *
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9: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq: *
10: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq: *
11: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq3: *
12: /cgn2_6/prodata/1/pubpna/us11_NEW_PUB.seq4: *
13: /cgn2_6/prodata/1/pubpna/us60_NEW_PUB.seq: *
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	159	16.0	990	US-10-793-626-413
2	159	16.0	2975	US-10-793-626-413
3	159	16.0	4114	US-10-793-626-4184
4	9.3	9.3	975	US-11-074-176-367
5	83.8	8.4	975	US-11-074-176-369
6	38.8	3.9	720	US-10-750-185-59863
7	38.8	3.9	720	US-10-750-185-59863
8	36.2	3.6	1272	US-11-096-568A-29311
9	35.8	3.6	583	US-09-925-065A-392869
10	35.4	3.6	419	US-09-925-065A-392870
11	35.4	3.6	419	US-09-925-065A-392870
12	35.4	3.6	5901	US-10-932-182A-2969
13	35.4	3.6	961	US-11-072-175-102
14	3.5	3.5	9	US-09-925-065A-392868
15	34.6	3.5	583	US-09-925-065A-392868
16	3.5	4429	7	US-10-753-195-9
17	34.2	3.4	583	US-09-925-065A-392870
18	34.2	3.4	1835	US-09-925-065A-45228
19	3.4	6	US-09-925-065A-45229	
20	3.4	6	US-09-925-065A-45230	

ALIGNMENTS

RESULT 1

US-10-793-626-413

; Sequence 413, Application US/10793626

; Publication No. Us20050255478A1

GENERAL INFORMATION:

; APPLICANT: KIMMEL, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS

; FILE REFERENCE: PU3480US

; CURRENT APPLICATION NUMBER: US/10793, 626

; PRIORITY FILING DATE: 2004-03-04

; PRIORITY APPLICATION NUMBER: 60/164, 258

; PRIORITY FILING DATE: 1999-11-09

; NUMBER OF SEQ ID NOS: 4472

; SOFTWARE: Patent Ver. 2.1

; SEQ ID NO: 413

; LENGTH: 990

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: nucleic acid sequence

; US-10-793-626-413

Query Match 16.0%; Score 159; DB 8; Length 990;

Best Local Similarity 49.8%; Pred. No. 2e-35; Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Oy Db 8 ATATGGTGTGCAAGTCAGTCTACATGGTGTCTATCCGGCTTACAGCTTA 61

Qy 62 TGGATTTCGATTCTCGCTGGGACAGGGTGTCTATCCGGCTTACAGCTTA 121

Db 68 TGGACTTCGATTGATTAATGTTATCCACCATGTTCCACGCCATTACTAC 127

Oy 122 ACATGAACTGAGGAAAGGCCATCACACAGCAGGGTTACGTTAGGAGA 181

Db 128 AATTTGATCTAGTCAGCATGGCTT-GATAATGTTTGTTGACAAATTAA 184

Oy 182 AACTTGGAATATATTATTGCGACGCGCATTAATGAAAGCGCTTTCTTGCGGGC 241

Db 185 AATGAGGAGTTAGATGTTGATGATGATAGGTTACGAAAGTTGACCA 244

APPLICANT: KIMMELLY, WILLIAM JOHN
 TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 FILE REFERENCE: PUS480US
 CURRENT APPLICATION NUMBER: US/10/793,626
 CURRENT FILING DATE: 2004-03-04
 PRIOR APPLICATION NUMBER: 60/164,258
 PRIOR FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 471
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 4184
 LENGTH: 4114
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-10-793-626-4184

Query Match 16.0%; Score 159; DB 8; Length 4114;
 Best Local Similarity 49.8%; Pred. No. 4e-35; Mismatches 455; Indels 6; Gaps 2;

Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Qy 2 ATATGTCACAAAGCTTACATGGAACTGCTACCGTAACGTATTAGAAGAACACA
 Db 1626 ATATGTCATCTCCATTCTTATACAAACACGTTACATTATTAGTAGAACACA 61
 Qy 62 TGGATTTCGATTCAGGGGGACAGAGGTGATCTATCGCGCGTTACAGCTGA 121
 Db 1686 TGGACTTGCAATTAAATGATATCCCAACCATGGTCCACGCCATATCAC 1745
 Qy 122 ACAGTGAGCTGACGGAGGCCATCAGACAGTCGGTTATCGGTATGGGAGA 1685
 Db 1746 AATTGATCTAGATCAGACATCGCTT--GAATGTTTGTGAAACAATTAA 1802
 Qy 182 AACCTGAAATAATTATTCGCGACCGCATATGAAAGGGTTATCTGTGGCGC 241
 Db 1803 AAGTAGGAGCTGTATAGATTGGTGTATGAAAGAAAGTTAGCTATTCAAC 1862
 Qy 242 TTATTTCCGAGCTATGGGAGTACGAAAAAAGATAAGGGAAAGATACGTCATCG 301
 Db 1863 ATTACTTCATGTCAGCTAACGCTACATGAACTTAAAGTTAGTTAACTAG 1922
 Qy 302 TCCCGCATGAGTTGTGACATGGTCTGTCTCGTCTGAAAGCTAAAG 361
 Db 1923 CACCTGAGGAGTTATGTTGGTTAGGTTAAATAAGTATTAGCGATTAAAC 1982
 Qy 362 AAAAGATCGATCTTACGTTAGAGAAAATAGATCTATGGATACAGTTAC 421
 .Db 1983 AAAGGTTAGAAATCATARTATGATGAAAMATACTGACTTGTATGTTCTC 2042
 Qy 422 CGCTTCACTGGATATGTCAGACCGGAGGGCGGAACCTGAGTAAAGAGCGAG 481
 Db 2043 CTTTACGTTCTGTCGACTGTGAAACAGGACATACGGTACCCATGAACTCAGATG 2102
 Qy 482 AGGGCTCAAACTGCTATGATATCAACCTGGTGTAGCAACGACGCCCACTTAT 541
 Db 2103 GTTATTAAATGTTAAAGATATTATGTTACATCTAACATGAACTTAAATTGATT 2162
 Qy 542 GGCACTAAACATCGCAGGAAATACAGGATACAGGATACAGCAAGGAAAG 601
 Db 2163 GGCATCTPATCTAATCTTAACTTACGCTTTTAACGCCACAGAAATCAAC 2222
 Qy 602 AGATGGCGGAGATTAGCCTTCTGCTTGGCCAAGGCTTGGAACTGTTGGCTCGGG 661
 Db 2223 TAATAGTTAAAGTGTGTAGATCATGGCTGTGAGCAGGAGAACATGGCT 2282
 Qy 662 GGGATATAACCCGCCCTCCCGGTGTCAGCTTGTGAGCTTGTGTTGGCTCGGG 721
 Db 2283 GTGGTTATCTCAACAGATGCTTATACCGCTACATTTAAAGACACAACTAGCT 2342
 Qy 722 CGCGCGCGATGAAAGGAAGGTGTACACCGCTTCTCAATTGGCAATATGAGCA 781
 Db 2343 GTTCCCTATAAGAAGTGAATATTATGATGTGTTAAAGTCTAGAATCAGTCAGTA 2402

RESULT 4
 US-11-074-176-367
 ; Sequence 367, Application US/11074176
 ; Publication No. US20050250135A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Klaenhammer, Todd R.
 ; APPLICANT: Russell, William M.
 ; APPLICANT: Altermann, Eric
 ; APPLICANT: McAuliffe, Olivia
 ; APPLICANT: Peril, Andrea Sacarne
 ; TITLE OF INVENTION: Nucleic Acid Sequences Encoding Stress-Related Proteins and Uses Thereof
 ; FILE REFERENCE: 5051-694
 ; CURRENT APPLICATION NUMBER: US/11/074,176
 ; CURRENT FILING DATE: 2005-03-07
 ; PRIOR APPLICATION NUMBER: 60/551,161
 ; PRIOR FILING DATE: 2004-03-08
 ; NUMBER OF SEQ ID NOS: 381
 ; SEQ ID NO: 367
 ; LENGTH: 975
 ; TYPE: DNA
 ; ORGANISM: Lactobacillus acidophilus
 ; FEATURE:
 ; NAME/KEY: CDS
 ; LOCATION: (1)..(975)
 ; FEATURE:
 ; NAME/KEY: misc_feature
 ; LOCATION: (0)..(0)
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 367
 ; LENGTH: 975
 Query Match 9.3%; Score 93; DB 12; Length 975;
 Best Local Similarity 46.4%; Pred. No. 2e-16; Mismatches 390; Indels 3; Gaps 1;

Matches 340; Conservative 0; Mismatches 390; Indels 3; Gaps 1;

Qy 197 TATTCGCGAGGGCATATTGAAAGGGTTATCTGTCGGCTTTATTTCCGGCT 256
 Db 188 TATATTGCAAGCTAAATGAAAGGTTAGGTATGGCTCGGGACTCTAACATCCGGAA 247
 Qy 257 ATGCGAGTACGAAAAAACGATACGGAGATACGGTACATGTCGCGATGAGTTG 316
 Db 248 ATGCTCATATTATGAGAAGAA--GAAATAAGATAATTATGCTTCTTGTGATTCA 304
 Db 188 TATATTGCAAGCTAAATGAAAGGTTAGGTATGGCTCGGGACTCTAACATCCGGAA 247
 Qy 317 TGACITGGGCTGTGAGTGTGAGCTTACGGTCTTGGAAAGCTAAAGAAAGTTCGACTT 376
 Db 305 TCCCTTGGATTAGGAGCTGTGAGCTTACGGTCTTGGAAAGCTAAAGTTCGACTT 364
 Qy 377 TAACGTTGAGAGAAAATTAGATCTTGTGAGTACAGTTACGGCTTACGTGAT 436
 Db 365 TCAACATGCCGATTAAATTCAAGGAAATGCAAGGCCCTCTCTCACTCGCTTA 424
 Qy 437 TGTCAAGCCGGACCGGCCGAACCTGACCAATGACAGAGAGACGCCCTCAAGTCT 496
 Db 425 TTGCAATAAACAGGTACATCATTTAGTGTGTTGAAAGACAAAGATGGATGCATT 484
 Qy 497 ATGATACTGCTGTGAGCTGAGGAGACGCCGACTTATGGCTGTAACCAAC 556
 Db 485 ATGATACTGCTGTGAGCTGAGGAGACGCCGACTTATGGCTGTAACCAAC 544

QY 557 TGCAGCAATTACAGGAATGAGCCGAASGAATTAGAGAGACAAGAGATGGGGGATAG 616
Db 545 TAATTACTATGCTGACGTATCTCCAAAATAGCTTAATAACTCTCGATAGATAAGTAA 604

QY 617 CCCTTCTGCTTTCGCCAACGGCTTAGAACATGTTGGTCGGCGGGATATACACCC 676
Db 605 ATATGCTGCTGCTACAGCCGGTGGATTAGGGCTCACACATACCAGGGTGGATCTG 664

QY 677 CTTCGGGTTGTCAGCTGTTATTGAAAGAACATCTAGAGGGGGCGATGAA 736
Db 665 AACAGCTTGTGAGTGTTCAATTAATTAAATTGTCGAATGTTGAAACCGAG 724

QY 737 CGAAGGTTGACAGCCGCTTCAATTGGCRAATATGACGATACCAAGGGCGAG 796
Db 725 AAGAAATATGATACTTACATCCTCACATTACATCGGTGAAACACACAAAGGACTG 784

QY 797 TGATTAACGGAGAGACGAAATTCAATTATCGCAATATACCTCGTGTGCAACGAA 856
Db 785 ATGAGTTGCCAACACTCAATTGATATCAATTGATGTCGAACTACATAGACA 844

QY 857 CTGGAACATATTCACACTATGACAACTGGCAAATCCAAAAGTAAATTATTC 916
Db 845 AAGGTTATTTCTACTACACCACTTCAACACAAATTACGTTGTTGATGAATA 904

QY 917 ATGAAACCTGTA 929
Db 905 AAGAGATCTAGA 917

RESULT 5
US-11-074-176-369 Application US/11074176
; Sequence 369, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAliffe, Olivia
; APPLICANT: Peril, Andrea
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; TITLE OF INVENTION: Stress-Related Proteins and Uses Thereof
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US11/074,176
; CURRENT FILING DATE: 2005-03-07
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 369
; LENGTH: 975
; TYPE: DNA
; ORGANISM: Lactobacillus acidophilus
; FEATURE: NAME/KEY: CDS
; LOCATION: (1)...(975)
; FEATURE: NAME/KEY: misc_feature
; LOCATION: (0)...(0)
; OTHER INFORMATION: ORF 1078; bshB
; US-11-074-176-369

Query Match 8.4%; Score 83.8; DB 12; Length 975;
Best Local Similarity 45.4%; Pred. No. 8-9e-14; Matches 341; Conservative 0; Mismatches 407; Indels 3; Gaps 1;

QY 181 AACCTGGAAATATATTGGCCGACGGATTANTGAGAMGGGTTATGCGGGG 240
Db 172 AATGATGATTAACCATATTATGATGCAATTAATGAAAGGGCTTGTGATGCGGA 231

QY 241 CTTATTTCCGGPATGGGAGTACGAAACATACCGGAGATACCGTCACT 300
Db 232 TAAATTTCAGG--TCCATTAATTCTTCCTAAATCGAAGGTAAGAAGATA 288

QY 301 GTCGGCGATGAGTTGTCGACATGGGTCTGTCAGTCCTCAGCTTGGAAAGAGCTAA 360
Db 289 GCTCTTTGAAATTAAGCCTACTTAAAGTAAATTGACGAGTTAA 348

QY 361 GAAAGATTCGACCTTACGTTGAGAAAATTAGATCTATTGATACAGTTA 420
Db 349 GAAATCTAGATATGCAATAATTAAATTAGCTTTGACCAATTATCCCTGCACT 408

QY 421 CCGCTTCACTGGATATGTCAGCCGAGGGCGAACCTGACGATGAGAACCGAGCA 480
Db 409 GATTACATGGATTAGTGTAAAGCTGTTAGGTGAACTAACCAT 468

QY 481 GACGCCCTCAAGSGCTATGATATCAACCTGGGTCAATGACGACAGCCCCGACTTTATA 540
Db 469 TCAGGTTACATATTATGATAATCCAGTGAATGTCCTACTACACATCTGAAATTCCG 528

QY 541 TGGCATGPRACCAATCTGCAATACAGGATCAGCGGAGCAATTAGGAA 600
Db 529 GATCATTAAATTAAATTAGTGTACTACCCGAGCTTACTCCACATACTCTAGAA 588

QY 601 GAGATGGGGATTAGCCCTTGCCTTGGCAAGGCTTGAAGCTTGAAGCTGTTGGCTCG 660
Db 589 TTGGTTCTTAATGTTGACCTTAACTATATASTAGAGACGCTTATTGAGAA 648

QY 661 GGCGATTATAACCGCCCTCCCGGTTGTCAGGCTTATTGAGAAACCTCTAGAG 720
Db 649 GGTGGATGATTCTGCTGATTGTTAGGTGATGTTGCTGGCACACTCCA 708

QY 721 CCGGCGCCGATGAAACGAAAGTGTACAGCGCTTTCAGTCATAATTGCAAAATTGACG 780
Db 709 CAAGGAAATAATGAGTGGAAATGTTACTAATTATTCATACTCGATCTGAGAA 768

QY 781 ATACCAAGGGCGACIGTATAAGGAAAGAGGAAGTCATTAATGCAATACTTCC 840
Db 769 CAACCTGATGGTTAGTGAAGTAAAGCAATTAATGCTATGATAATGATACAGAT 828

QY 841 GTGATGTCGAAAGGAAACTGGAACACTAATTCACCACTATGACATGGCAAATCCAA 900
Db 829 TGTATGAACTTAGATAAGGTTATGTTACTCTATGACAAATCGATTAAT 888

QY 901 AAAGPAAATTTCATCAGAACCTGACT 931
Db 889 GCAGTAGATATGCTATAACGAGATTAGATT 919

RESULT 6
US-10-750-183-59863/C
; Sequence 59863, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMI GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: BARTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MM11.00-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO 59863
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Bovine 19866881284323
; US-10-750-183-59863
Query Match 3.9%; Score 38.8; DB 8; Length 720;

Best Local Similarity 57.4%; Pred. No. 0.7; Mismatches 52; Indels 0; Gaps 0;
 Matches 70; Conservative 0; ;

QY 824 ATAGCGATAATACCTCCGATGTCGAACGAACTGGRAGACTATTTCCACACTAG 883
 Db 262 ATACCAATGGTGTGATGCTATTTATCATGCAAGTATTTATACATAC 203
 QY 884 ACAATCGGAAATCCAAAAGTAATTTTCTGAGAACCTTGACTGTTGGAGCTA 943
 Db 202 ACATCTGGCTAATAGAATGGCATTTTATTCAAGTGTGCTAACCTC 143
 QY 944 AA 945
 Db 142 AA 141

RESULT 7
 US-10-750-623-59863/c
 Sequence 59863, Application US/10750623
 Publication No. US20050287531A1.

GENERAL INFORMATION:
 APPLICANT: MMI GENOMICS, INC.
 APPLICANT: DENISE, Sue K.
 APPLICANT: KERR, Richard
 APPLICANT: ROSENFIELD, David
 APPLICANT: HOLM, Tom
 APPLICANT: BATES, Stephen
 APPLICANT: FANTIN, Dennis

TITLE OF INVENTION: METHODS AND SYSTEMS FOR INFERRING BOVINE TRAITS
 FILE REFERENCE: WO1100-1
 CURRENT APPLICATION NUMBER: US/10/750,623
 CURRENT FILING DATE: 2003-12-31
 PRIOR APPLICATION NUMBER: US 60/437,482
 PRIOR FILING DATE: 2002-12-31
 NUMBER OF SEQ ID NOS: 64922
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 59863
 LENGTH: 720
 ORGANISM: Bovine 19866881284323

US-10-750-623-59863

Query Match 3.9%; Score 38.8; DB 8; Length 720;
 Best Local Similarity 57.4%; Pred. No. 0.7; Mismatches 52; Indels 0; Gaps 0;
 Matches 70; Conservative 0; ;

QY 824 ATACGCRATAPCTTCCGTGAGTGCACCGAACACTGAACTTCCACCATG 883
 Db 262 ATACCAATGGTGTGATGCTATTTATCATGCAAGTATTTATACATAC 203
 QY 884 ACAATCGGAAATCCAAAAGTAATTTTCTGAGAACCTTGACTGTTGGAGCTA 943
 Db 202 ACATCTGGCTAATAGAATGGCATTTTATTCAAGTGTGCTAACCTC 143
 QY 944 AA 945
 Db 142 AA 141

RESULT 8
 US-11-096-568A-29311
 ; Sequence 29311, Application US/11096568A
 ; Publication No. US20060048240A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Alexandrov, Nikolai et al.
 ; TITLE OF INVENTION: Sequence-Determined DNA Fragments and Corresponding Polypeptides
 ; TITLE OF INVENTION: Therry
 ; FILE REFERENCE: 2750-1592PUS2
 ; CURRENT APPLICATION NUMBER: US/11/096,568A
 ; NUMBER OF SEQ ID NOS: 34471
 ; SEQ ID NO: 29311
 ; LENGTH: 1272

RESULT 9
 US-09-925-065A-392869/c
 Sequence 392869, Application US/09925065A
 Publication No. US20040181040A1

GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827-135
 CURRENT APPLICATION NUMBER: US/09/925, 065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243, 096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252, 147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250, 092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261, 766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289, 846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957056
 SOFTWARE: FASTSEQ for Windows Version 4.0
 SEQ ID NO: 392869

TYPE: DNA
 ORGANISM: Arabidopsis thaliana
 FEATURE:
 NAME/KEY: misc_feature
 LOCATION: (1)..(1272)
 OTHER INFORMATION: Ceres Seq. ID no. 4809357
 ; US-11-096-568A-29311

Query Match 3.6%; Score 36.2; DB 9; Length 1272;
 Best Local Similarity 57.5%; Pred. No. 5.2; Mismatches 48; Indels 0; Gaps 0;
 Matches 65; Conservative 0; ;

QY 149 AGACACAGTACGGTTAACGGTATGGAGAACCTGGAAATAATTATTGCCGACG 208
 Db 419 AGACTGACCTTGGTCTCGATGAGTAGCTACAAGCTGTGATTCCTGCGCT 478
 QY 209 GCATTAATGAAAGCGGTTATCTGTGCGCTTTATTCCGGGTATGG 261
 Db 479 GCTCAATGGTACCGATGAACTCTCCGGCCTTACATCTTACAGTTGIG 531

RESULT 10
 US-09-925-065A-654182
 Sequence 654182, Application US/09925065A
 Publication No. US20040181040A1
 GENERAL INFORMATION:
 APPLICANT: Wang, David G.

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925,065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-03-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 654182
 LENGTH: 419
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-654182

Query Match 3.6%; Score 35.4; DB 6; Length 419;
 Best Local Similarity 57.8%; Pred. No. 5.1; Mismatches 0; Gaps 0;
 Matches 63; Conservative 0; Indels 0; Gaps 0;

Qy 333 AGTCGTCATCTTGAAACAGTAAAGAAAGATTGATCTTAACTGGATGAGAA 392
 Db 244 AGATTAACGAAATTAGAAACAGATAATTAGATAAACTGACCATTTATGAA 303

Qy 393 AAATTAGATCTATGGATACGTTACCGCTTCACTGGATATGTC 441
 Db 304 TAAATTAGATGAAACGATTATTTCTCCAACTGTAAATTGTTA 352

RESULT 11
 US-09-925-065A-654183
 ; Sequence 655183, Application US/09925065A
 ; Publication No. US2004181048A1
 ; GENERAL INFORMATION:
 APPLICANT: Wang, David G.
 TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108827.135
 CURRENT APPLICATION NUMBER: US/09/925,065A
 PRIOR APPLICATION NUMBER: US 60/243,096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252,147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250,092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261,766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289,846
 PRIOR FILING DATE: 2001-03-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 654183
 LENGTH: 419
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-654183

Query Match 3.6%; Score 35.4; DB 6; Length 419;
 Best Local Similarity 57.8%; Pred. No. 5.1; Mismatches 0; Gaps 0;
 Matches 63; Conservative 0; Indels 0; Gaps 0;

Qy 333 AGTCGTCATCTTGAAACAGTAAAGAAAGATTGATCTTAACTGGATGAGAA 392
 Db 244 AGATTAACGAAATTAGAAACAGATAATTAGATAAACTGACCATTTATGAA 303

RESULT 12
 US-10-932-182A-2969
 ; Sequence 2969, Application US/10932182A
 ; Publication No. US20060046253A1
 ; GENERAL INFORMATION:
 APPLICANT: NAKAMURA, NORIHIRO
 APPLICANT: KODAMA, YUKIKO
 APPLICANT: FUJIMURA, TOMOKO
 APPLICANT: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: 030685-043
 CURRENT APPLICATION NUMBER: US/10/932,182A
 PRIOR FILING DATE: 2004-03-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 2969
 LENGTH: 5901
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-2969

Query Match 3.6%; Score 35.4; DB 7; Length 5901;
 Best Local Similarity 50.9%; Pred. No. 19; Mismatches 81; Indels 0; Gaps 0;
 Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 693 AGCTTGTTTATGGAAAGAACATCTAGAGCGGGCGCGATGAAACGAAGGTGACAGC 752
 Db 894 AGCTTTACAGGATGAAATTAGTGATTCGGCTACAGGTGCAAGTAAACAGA 953

Qy 813 CGAAATTCTATACGAAATACTTCCGTGATGTCAGGAAAC 812
 Db 1014 CGAAATTCTATACGAAATACTTCCGTGATGTCAGGAAAC 1058

RESULT 13
 US-10-932-182A-2969
 ; Sequence 2969, Application US/10932182A
 ; Publication No. US20060046253A1
 ; GENERAL INFORMATION:
 APPLICANT: NAKAO, YOSHIHIRO
 APPLICANT: NAKAMURA, NORIHIRO
 APPLICANT: KODAMA, YUKIKO
 APPLICANT: FUJIMURA, TOMOKO
 APPLICANT: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: 030685-043
 CURRENT APPLICATION NUMBER: US/10/932,182A
 CURRENT FILING DATE: 2004-09-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: PatentIn version 3.3
 SEQ ID NO: 2969
 LENGTH: 5901
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-2969

Query Match 3.6%; Score 35.4; DB 7; Length 5901;
 Best Local Similarity 50.9%; Pred. No. 19; Mismatches 81; Indels 0; Gaps 0;
 Matches 84; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

Qy 693 AGCTTGTTTATGGAAAGAACATCTAGAGCGGGCGCGATGAAACGAAGGTGACAGC 752
 Db 894 AGCTTTACAGGATGAAATTAGTGATTCGGCTACAGGTGCAAGTAAACAGA 953

QY 753 CGCTTTCAATTGGCAATATGCGATAACCAAGGCGACTGATACGGAGAGA 812
; ;
; ;
Db 954 CGTGCACCTACGTATTAACAGCGTAACAGTTCCTCGATCACGGAAA 1013
; ;
QY 813 CGAATTCTTACGCAATATACCTCCGTGATGCGAAC 877
; ;
Db 1014 CGAAATTGATACATACGATAGTTCAAGGTTCTACGTAGC 1058
; ;
; ;

RESULT 14
US-11-072-175-102
; Sequence 102, Application US/11072175
; Publication No. US20060029944A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT
; FILE REFERENCE: D0273A CIP
; CURRENT APPLICATION NUMBER: US/11/072, 175
; CURRENT FILING DATE: 2005-03-05
; PRIOR APPLICATION NUMBER: US 60/406, 385
; PRIOR FILING DATE: 2002-08-27
; PRIOR APPLICATION NUMBER: US 10/648, 593
; PRIOR FILING DATE: 2003-08-26
; NUMBER OF SEQ ID NOS: 571
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 102
; LENGTH: 961
; TYPE: DNA
; ORGANISM: Homo sapiens
; US-11-072-175-102

Query Match 3.5%; Score 34.6; DB 6; Length 583;
; Best Local Similarity 49.7%; Pred. No. 10;
; Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
; ;
Qy 802 ACGGAGAGAGCAATTCAATTACCCAAATTACTTCGCGATGTCGAACTCGA 861
; ;
Db 341 ATGGAGAGCTTAATGTTATCCAGTAAGAGACATCTGAAGAGCTGATA 282
; ;
Qy 862 AACATCATTTCCACCACTATGACAATGGCAAATCCAAGAATTATTCATGA 921
; ;
Db 281 CGATATGATCAACTATGACATTCACAAAAACCACTAAATGTAATAA 222
; ;
Qy 922 GACCTGAGCTGTTGAGCTTAAGTGTTCGCTAAAGCAGAGAGATCAT 978
; ;
Db 221 GATCAGTGTGCCAGGGAAAACGGGGRTGACAGGTGCGCACAGGATCT 165
; ;

Query Match 3.5%; Score 34.6; DB 6; Length 583;
; Best Local Similarity 49.7%; Pred. No. 10;
; Matches 88; Conservative 0; Mismatches 89; Indels 0; Gaps 0;
; ;
Qy 802 ACGGAGAGAGCAATTCAATTACCCAAATTACTTCGCGATGTCGAACTCGA 861
; ;
Db 341 ATGGAGAGCTTAATGTTATCCAGTAAGAGACATCTGAAGAGCTGATA 282
; ;
Qy 862 AACATCATTTCCACCACTATGACAATGGCAAATCCAAGAATTATTCATGA 921
; ;
Db 281 CGATATGATCAACTATGACATTCACAAAAACCACTAAATGTAATAA 222
; ;
Qy 922 GACCTGAGCTGTTGAGCTTAAGTGTTCGCTAAAGCAGAGAGATCAT 978
; ;
Db 221 GATCAGTGTGCCAGGGAAAACGGGGRTGACAGGTGCGCACAGGATCT 165
; ;

Search completed: March 18, 2006, 12:06:10
Job time : 453 secs

RESULT 15
US-19-922-065A-392868/C
; Sequence 392868, Application US/09925065A
; Publication No. US20040181048A1
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single
; Nucleotide Polymorphisms in the Human Genome
; FILE REFERENCE: 108827..135
; CURRENT APPLICATION NUMBER: US/09/925, 065A
; CURRENT FILING DATE: 2001-08-08
; PRIOR APPLICATION NUMBER: US 60/243, 096
; PRIOR FILING DATE: 2000-10-24
; PRIOR APPLICATION NUMBER: US 60/252, 147
; PRIOR FILING DATE: 2000-11-20
; PRIOR APPLICATION NUMBER: US 60/250, 092
; PRIOR FILING DATE: 2000-11-30
; PRIOR APPLICATION NUMBER: US 60/261, 766

RESULT 2		TITLE	
LOCUS	D45912	JOURNAL	Cloning and nucleotide sequencing of a 15 kb region of the <i>Bacillus subtilis</i> genome containing the iol operon
DEFINITION	23351 bp DNA linear BCT 10-FEB-1999	PUBLMED	Microbiology 140 (Pt 9), 2289-2298 (1994)
ACCESSION	Bacillus subtilis genome sequence between the iol and hut operon, partial and complete cds.	REFERENCE	795281
VERSION	D45912	AUTHORS	2 (sites)
KEYWORDS	partial and complete cds.	Yoshida, K., Sano, H., Seki, S., Oda, M., Fujimura, M. and Fujita, Y.	
	D45912.1 GI:11408482	TITLE	Cloning and sequencing of a 29 kb region of the <i>Bacillus subtilis</i> genome containing the hut and wapa loci
SOURCE	Bacillus subtilis	JOURNAL	Microbiology 141 (Pt 2), 337-343 (1995)
ORGANISM	Bacillus subtilis	PUBLMED	7704283
REFERENCE	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus;	REFERENCE	3 (sites)
AUTHORS	1 (sites)	AUTHORS	Yoshida, K., Fujimura, M., Yanai, N. and Fujita, Y.
		TITLE	Cloning and sequencing of a 23-kb region of the <i>Bacillus subtilis</i> genome between the iol and hut operons
		JOURNAL	DNA Res. 2 (6), 295-301 (1995)
		PUBLMED	8867804
		REFERENCE	4 (bases 2202 to 23351)
		AUTHORS	Saxild, H.H., Andersen, L.N. and Hammer, K.
		TITLE	Dra-nupC-Pop operon of <i>Bacillus subtilis</i> : nucleotide sequence, induction by deoxyribonucleosides, and transcriptional regulation by the deoR-encoded DeoR repressor protein
		JOURNAL	J. Bacteriol. 178 (2), 424-434 (1996)
		PUBLMED	8550462
		REFERENCE	5 (bases 1 to 23351)
		AUTHORS	Fujita, Y.
		TITLE	Direct Submission
		JOURNAL	Submitted (10-FEB-1995) Yasutaro Fujita, Fukuyama University, Biotechnology, 985 Sanzo, Higashimura-cho, Fukuyama, Hiroshima 729-02, Japan (E-mail: yfujita@fubt.fukuyama-u.ac.jp, Tel: 0849-36-2023)
		FEATURES	
		source	
		gene	
		CDS	
			1.. .657
			/gene="yxdK"
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			/note="belongs to the histidine protein kinase family of adaptive responses in Bacteria"
			/citation=[1]
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			/transl_table=11
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			/citation=[1]
			/codon_start=1
			/transl_table=11
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			/ab_xref="GI:1403484"
			/translation="MANNLEVKINKTYKGQVISYQALKOISFSEEGETAVMGPSGSKTYLWISTIDRPDSGLILNGENPKRKTKLHRKRQGFVFQDFNLQDMLTIGENIMDPLTKEPSWMEKKGIAAKLGILNENKTFEPVAGGORORALARVHRSQSLADEPTGKLSKDKDVKDNTQSLRNDVHATMIVDHPVSAJCRVVIKDQVLPNEYTRGENQVFBQDVLMLGGNNANDLSSVRL"
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			/gene="yxdL"
			1549.. .3417
			/gene="yxdM"

QY	8854	CGCTTCACTGGTTATCAGACGAGCCGAACTTGAGCTAGAACAGAGCA	8913
QY	481	GACGGCTCAAGTCTGTATGATACCTGGTGTGATGACGACGCCACTTATA	540
QY	8914	GACGGCTCAAGTCTGTATGATACCTGGTGTGATGACGACGCCACTTATA	8973
QY	541	TGGCATGACCATTCGAGCATATCAGGATACAGGATAGACGAGCAATTAGAGCAA	600
Db	8974	TGGCATGACCATTCGAGCATATCAGGATACAGGATAGACGAGCAATTAGAGCAA	9033
QY	601	GAGATGGCGGAGTAGCCTTGTCTTGCCASGCTTAGGAACGTGTTGGTCCTCCG	660
QY	9034	GAGATGGCGGAGTAGCCTTGTCTTGCCASGCTTAGGAACGTGTTGGTCCTCCG	9093
QY	661	GGGGATATACACCGCTCCGGTTTCAGGCTGTATTGAGAACATCAGAG	720
Db	9094	GGGGATATACACCGCTCCGGTTTCAGGCTGTATTGAGAACATCAGAG	9153
QY	721	CCGGGGCGATGAAAGAAGGTGTAACGGAGAGGAAATCTAATTGGCAATATGACG	780
QY	9154	CCGGGGCGATGAAAGAAGGTGTAACGGAGAGGAAATCTAATTGGCAATATGACG	9213
QY	781	ATPACCAAGGGCCGATGAAAGGAAATCTAATTGGCAATATGACG	840
QY	9214	ATPACCAAGGGCCGATGAAAGGAAATCTAATTGGCAATATGACG	9273
QY	841	GTGATGCGAACGAACTACTTACATTGACACTATGACATGGAAATCCA	900
Db	9274	GTGATGCGAACGAACTACTTACATTGACACTATGACATGGAAATCCA	9333
QY	901	AAAGTAAATTATTTCATGAGAGCTTGACTGTTGGAGCTAAAGTGTTCGCTAA	960
Db	9334	AAAGTAAATTATTTCATGAGAGCTTGACTGTTGGAGCTAAAGTGTTCGCTAA	9393
QY	961	GCAGAGAGAGATTCATGAGCTTAA	990
Db	9394	GCAGAGAGAGATTCATGAGCTTAA	9423
RESULT 3			
BSUB0021/c	BSUB0021	203901 bp	DNA linear BCT 18-APR-2005
LOCUS	Bacillus subtilis complete genome	(section 21 of 21):	From 4010730 to 4214630.
DEFINITION	Bacillus subtilis complete genome	(section 21 of 21):	From 4010730 to 4214630.
ACCESSION	Z99124	AL009126	Z99124.2 GI:32468840
VERSION			
KEYWORDS			
ORGANISM	Bacillus subtilis subsp. subtilis str. 168		
SOURCE	Bacillus subtilis subsp. subtilis str. 168		
Bacteria: Firmicutes; Bacillales; Bacillaceae; Bacillus.			
Bacterium: Firmicutes; Bacillales; Bacillaceae; Bacillus.			
REFERENCE	1 (bases 1 to 203901)		
AUTHORS	Kunst, F., Ogasawara, N., Moszer, I., Albertini, A.M., Alloni, G., Azevedo, V., Bertler, M.G., Bessieres, P., Bolotin, A., Borchart, S., Borris, R., Bourrier, L., Brans, A., Braun, M., Brignell, S.C., Bron, S., Brouillet, S., Bruschi, C.V., Caldwell, B., Capuano, V., Carter, N.M., Choi, S.K., Codani, J.J., Connerton, I.F., Cummings, N.J., Daniel, R.A., Denizot, P., Devani, K.M., Dusthoff, A., Erlich, S.D., Ellerbeck, P.T., Entian, K.D., Errington, J., Fabret, C., Ferrari, E., Foulger, D., Fritz, C., Fujita, M., Fujita, Y., Fuma, S., Galizzi, A., Galleon, N., Ghim, S.Y., Glaser, P., Goffeau, A., Golightly, E.J., Grandi, G., Guiseppi, G., Guy, B.J., Haga, K., Haleck, J., Harwood, C.R., Henaut, A., Hilbert, H., Holzapfel, S., Hobson, S., Hull, M.F., Itaya, M., Jones, I.D., Jones, B., Karimata, D., Kasahara, Y., Klaerr, Blanchard, M., Klein, C., Kobayashi, Y., Koettner, P., Koningsstein, G., Krogh, S., Kumano, M., Kurita, K., Lapinus, A., Lardinois, S., Lauber, J., Lazarev, V., Lee, S.M., Levine, A., Liu, H., Masuda, S., Mauel, C., Medigue, C., Medina, N., Meliado, R.P., Mizuno, M., Moestl, D., Nakai, S., Noback, M., Noone, D., O'Reilly, M., Ogawa, K., Ogiwara, I., Oudega, B., Park, S.H., Parro, V., Pohl, T.M., Portetelle, D., Porwollik, S., Prescott, A.M., Presecan, E., Pujic, P., Purvelle, B., Rapoport, G., Rey, M., Reynolds, S., Rieger, M., Rivolle, C., Rocha, E., Roche, B., Ross, M., Sadaie, Y., Sato, T., Scanlan, E., Schleicher, S., Schroeter, R., Scorzoni, F., Sekiguchi, J.,		
FEATURES			
SOURCE			
COMMENT	On July 7, 2003 this sequence version replaced gi:2636442. This entry contains data from release R16.1 of the Subtilist database. Further data on gene annotation and detailed information about changes from previous releases can be found at http://genolist.pasteur.fr/Subtilist/ .		
LOCATION	Location/Qualifiers		
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	/strain="168"		
	/db_xref="taxon:224308"		
	/complement("131..859")		
	/gene="bglS"		
	/locus_tag="BSU139070"		
	/complement("131..859")		
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	/locus_tag="BSU139070"		
	/EC_number="3.2.1.73"		
	/function="lichenan degradation"		
	/note="alternate gene name: bgl, lics"		
	/codon_start=1		
	/transl_table=1		
	/product="endo-beta-1,3-1,4 glucanase"		
	/protein_id="CAB15943.1"		
	/db_xref="IGI:2636453"		
	/db_xref="GOA:PO4957"		
	/db_xref="InterPro:IPR000757"		
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	/locus_tag="BSU139080"		
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	/gene="lictm"		
	/locus_tag="BSU139080"		
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	/transl_table=11		
	/product="transcriptional antiterminator (Bg1G family)"		
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	/db_xref="GO:PO49805"		
	/db_xref="Subtilist:BG10474"		
	/db_xref="UniProt:Swiss-Prot:P39805"		

/translation="MKI AKV INNNIVI SVNEQ KELVINGRLAQOKSGDDDEBARI
EKVITLNDKOVSEKEKILUDIPICMESEBETHYAKUOLGKUNDSTYVSTDHIN
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VNASLANEEHENPINITKVKMELSLVKHKELESLVYKVUTKFAORLFLNG
THMESQDDILDTURGEKTHAYECIKKIOYIEKEYERKLTSEBLLYLTTHIRUVKO
A" complement (2084. . 2764)

gene

/gene="yxiP"

/locus tag="BSU39090"

/complement (2084. . 2764)

CDS

/gene="yxiP"

/locus tag="BSU39090"

/function="unknown"

/note="similar to unknown proteins"

/codon_start=1

/transl_table=11

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/db_xref="GI:2636455"

/db_xref="InterPro:IPR00437"

/db_xref="SubJlist:BG11145"

/db_xref="UniProt:Swiss-Prot:P42307"

/translations="MRIGLCLLIVLWMSCESEAQMADCKTVKOTAAKP
MSKKKKDQFQALASDROLAIVFSSMIQNSEAFPIYGIGNPYEFFRISMEEADIAKEN
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2971. . 4257

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/note="similar to unknown proteins"

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LISIAVILLAOQATIPYVSUSYFASIFLAWWGLTIPMKHVHORYYKKEPHIV
INSFKRIGOTMGRIROYALEFLYLAYFIDCGVHTIMTSYSDLGISSSLII
LFTVQVIAFPFELIYKGKLAERFGKTMVYVJYVIMPCVVAWMETTDWILAMLV
AVFSLTLFVGIVVIALFVPESTSTDVSOQNDLPL"

complement (4276. . 5715)

/gene="dead"

/locus_tag="BSU39110"

/complement (4276. . 5715)

CDS

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/locus tag="BSU39110"

/note="Alternative gene name: yxiN"

/codon_start=1

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/db_xref="SubJlist:BG11143"

/db_xref="UniProt:Swiss-Prot:P42305"

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gene

/locus tag="BSU39120"

/function="unknown"

/note="similar to rhamnogalacturonan acetyl esterase"

/codon_start=1

/transl_table=11

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/db_xref="UniProt:IPR008994"

/db_xref="SubJlist:BG11142"

/db_xref="UniProt:Swiss-Prot:P42304"

Query Match

Qy	Match	Score	DB	Length
Db	1 CATATGGCACAGCTTACATGGAACCTGCTAACCTGAAACATGATTAGCAGAAC	98.3%	1	203901
Qy	2971 AACATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	99.3%	1	203901
Db	51819 CAAATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	98.3	1	203901
Qy	51819 AACATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	99.3	1	203901
Db	51699 AATATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	98.3	1	203901
Qy	51699 AATATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	99.3	1	203901
Db	51759 ATGGATTTCGCAATTCTAGCTGGGACAGGGTATTCTCTATCCGGCGTACAGCTG	98.3	1	203901
Qy	51759 ATGGATTTCGCAATTCTAGCTGGGACAGGGTATTCTCTATCCGGCGTACAGCTG	99.3	1	203901
Db	51639 AACATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	98.3	1	203901
Qy	51639 AACATGTTGCAAGCTTCATGGAACACTGCTAACATGATTAGCAGAAC	99.3	1	203901
Db	51640 CTTTATTTCCGGCTATCCGGGATCGAAACAAACGCTACGGGAGAACCGTTATCTGTGGGG	98.3	1	203901
Qy	51640 CTTTATTTCCGGCTATCCGGGATCGAAACAAACGCTACGGGAGAACCGTTATCTGTGGGG	99.3	1	203901
Db	51579 CTTTATTTCCGGCTATCCGGGATCGAAACAAACGCTACGGGAGAACCGTTATCTGTGGGG	98.3	1	203901
Qy	51579 CTTTATTTCCGGCTATCCGGGATCGAAACAAACGCTACGGGAGAACCGTTATCTGTGGGG	99.3	1	203901
Db	51519 GTCGCCGATGATGTTGAGCATGGTCTCTGCTAGCTTGTTGAGAGCTAA	98.3	1	203901
Qy	51519 GTCGCCGATGATGTTGAGCATGGTCTCTGCTAGCTTGTTGAGAGCTAA	99.3	1	203901
Db	51519 GAAAGATTCGATCTTACAGTTGAGAGAAAATAGACGTTATGGATACGTTTA	98.3	1	203901
Qy	51519 GAAAGATTCGATCTTACAGTTGAGAGAAAATAGACGTTATGGATACGTTTA	99.3	1	203901
Db	51459 GAAAGATTCGATCTTACAGTTGAGAGAAAATAGACGTTATGGATACGTTTA	98.3	1	203901
Qy	51459 GAAAGATTCGATCTTACAGTTGAGAGAAAATAGACGTTATGGATACGTTTA	99.3	1	203901
Db	51339 CGCGTTCTCTGGATATTCTAGACGCCAGGGCCGAAACTGAGATAGAACCAAGAGCA	98.3	1	203901
Qy	51339 CGCGTTCTCTGGATATTCTAGACGCCAGGGCCGAAACTGAGATAGAACCAAGAGCA	99.3	1	203901
Db	51340 TGGCATGTTACCATCTGCAGCATATAACGAACTGAGATAGAACCAAGAGCA	98.3	1	203901
Qy	51340 TGGCATGTTACCATCTGCAGCATATAACGAACTGAGATAGAACCAAGAGCA	99.3	1	203901
Db	51279 TGGCATGTTACCATCTGCAGCATATAACGAACTGAGATAGAACCAAGAGCA	98.3	1	203901
Qy	51279 TGGCATGTTACCATCTGCAGCATATAACGAACTGAGATAGAACCAAGAGCA	99.3	1	203901
Db	601 GAGATGGCGGATAGGCCCTTCGCTTGGCAAGCTTAGAGACTGTTGCTCCGG	98.3	1	203901
Qy	601 GAGATGGCGGATAGGCCCTTCGCTTGGCAAGCTTAGAGACTGTTGCTCCGG	99.3	1	203901
Db	51219 GAGATGGCGGATAGGCCCTTCGCTTGGCAAGCTTAGAGACTGTTGCTCCGG	98.3	1	203901
Qy	51219 GAGATGGCGGATAGGCCCTTCGCTTGGCAAGCTTAGAGACTGTTGCTCCGG	99.3	1	203901
Db	661 GGGGATATAACGCCCTCCGGTTGTCAGAGCTTTTGAAGAACATCTGAG	98.3	1	203901
Qy	661 GGGGATATAACGCCCTCCGGTTGTCAGAGCTTTTGAAGAACATCTGAG	99.3	1	203901

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GNIGKALSFVTAKEPKRDLIERYTGPFLPKRAPSQEVAKPFLAKNDRPES
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/locus tag="BSU39120"

/function="unknown"

/note="similar to rhamnogalacturonan acetyl esterase"

/codon_start=1

/transl_table=11

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/db_xref="InterPro:IPR001087"

/db_xref="UniProt:IPR008994"

/db_xref="SubJlist:BG11142"

/db_xref="UniProt:Swiss-Prot:P42304"

Db	51159	GGGGATPATACACCGCTTCCCGTTGTCAGAGCTTATTGAAAGAACATCTAGAG	51100	Query Match 44.2%; Score 440; DB 1; Length 11000; Best Local Similarity 65.2%; Pred. No. 2.4e-108; Matches 647; Conservative 0; Mismatches 345; Indels 0; Gaps -0;
Qy	721	CGGGGGCCGATGAAACGAAAGGTGAAAGCCGTTCAATTGGCAAATGAGC	780	
Db	51099	CGGGGGCGATGAAACGAAAGGTGAAAGCCGTTCAATTGGCAAATGAGC	51040	
Qy	781	ATACCAAGGCCAGTAAACGGAGAGCAATTCAGCTTACCGTAAACTGTCACGGCTTCAATTGGCAAATGAGC	840	
Db	51039	ATACCAAGGCCAGTAAACGGAGAGCAATTCAGCTTACCGTAAACTGTCACGGCTTCAATTGGCAAATGAGC	50980	
Qy	841	GTCATGTCACAACTGAAACTACTATTCCACCATATGAAATGGCAATTCGA	900	
Db	50979	GTCATGTCACAACTGAAACTACTATTCCACCATATGAAATGGCAATTCGA	50920	
Qy	901	AAGTAATTATTTCATGAGACCTTGACTGTTGGAGCTAATGTTCCCTAA	960	
Db	50919	AAGTAATTATTTCATGAGACCTTGACTGTTGGAGCTAATGTTCCCTAA	50860	
Qy	961	GCAGAGAGAGAGATTCATGCTTAAAGTGTTCGCTAA	990	
Db	50859	GCAGAGAGAGAGATTCATGCTTAAAGTGTTCGCTAA	50830	
RESULT 4				
WPCOMMENT	40/c			
Sequence Split into 43 fragments LOCUS AE017333 Accession AE017333				
Fragment Name				
Begin	End			
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AE017333_01	100001	210000		
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AE017333_03	300001	410000		
AE017333_04	400001	510000		
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AE017333_06	600001	710000		
AE017333_07	700001	810000		
AE017333_08	800001	910000		
AE017333_09	900001	1010000		
AE017333_10	100001	1110000		
AE017333_11	1100001	1210000		
AE017333_12	1200001	1310000		
AE017333_13	1300001	1410000		
AE017333_14	1400001	1510000		
AE017333_15	1500001	1610000		
AE017333_16	1600001	1710000		
AE017333_17	1700001	1810000		
AE017333_18	1800001	1910000		
AE017333_19	1900001	2010000		
AE017333_20	2000001	2110000		
AE017333_21	2100001	2210000		
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AE017333_35	3500001	3610000		
AE017333_36	3600001	3710000		
AE017333_37	3700001	3810000		
AE017333_38	3800001	3910000		
AE017333_39	3900001	4010000		
AE017333_40	4000001	4110000		
AE017333_41	4100001	4210000		
AE017333_42	4200001	4222645		

RESULT 5	
CP000002_40/c	
WPCOMMENT	
Fragment	split into 43 fragments
Name	LOCUS CP000002 Accession CP000002
Begin	1
End	110000
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CP000002_02	310000
CP000002_03	410000
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CP000002_05	510000
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CP000002_10	1010000
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CP000002_12	1210000
CP000002_13	1310000
CP000002_14	1410000
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CP000002_16	1610000
CP000002_17	1710000
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CP000002_33	3310000
CP000002_34	3410000
CP000002_35	3510000
CP000002_36	3610000
CP000002_37	3710000
CP000002_38	3810000
CP000002_39	3910000
CP000002_40	4010000
CP000002_41	4110000
CP000002_42	4210000
CP000002_43	4221334

Continuation 741 of 43) of CP000002 from base 4000001 (CP000002 Bacillus licheniformis)

RESULT 6	
AX433304	
LOCUS AX433304	
DEFINITION	Sequence 1719 from Patent WO0229113.
VERSION	AX433304_1 GI:21658108
KEYWORDS	Bacillus licheniformis
SOURCE	Bacillus licheniformis
ORGANISM	Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
REFERENCE	1. Berka, R. and Clausen, I. G. Methods for monitoring multiple gene expression Patient: Wo 022911-A 17/9 11-APR-2002; Novozymes Biotech, Inc. (US); Novozymes A/S (DK) Location/Qualifiers /organism="Bacillus licheniformis" /mol_type="unassigned DNA" /db_xref="taxon:1402"
AUTHORS	
TITLE	
JOURNAL	
FEATURES	
source	
ORIGIN	
Query Match	44.2%; Score 439.8; DB 6; Length 990;

AE017225_35/c
WPCOMMENT

Sequence split into 53 fragments	LOCUS	AE017225	Accession	AE017225
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AE017225_02	200001	310000		
AE017225_03	300001	410000		
AE017225_04	400001	510000		
AE017225_05	500001	610000		
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AE017225_09	900001	1010000		
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AE017225_12	120001	1310000		
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AE017225_40	400001	4110000		
AE017225_41	410001	4210000		
AE017225_42	420001	4310000		
AE017225_43	430001	4410000		
AE017225_44	440001	4510000		
AE017225_45	450001	4610000		
AE017225_46	460001	4710000		
AE017225_47	470001	4810000		
AE017225_48	480001	4910000		
AE017225_49	490001	5010000		
AE017225_50	500001	5110000		
AE017225_51	510001	5210000		
AE017225_52	520001	5228663		
Continuation (36 of 53) of AE017225 from base 3500001 (AE017225 Bacillus anthracis str				
Query Match	29.4%	Score	293.2;	DB 1;
Best Local Similarity	55.9%;	Pred.	No. 1.9e-68;	Length 110000;
Matches	556;	Conservative	0;	Mismatches 438; Indels 0; Gaps 0;
Qy	3	TATGTCAGGTCTTACATGGAACTAAGTAACTGTTAGCAAGAACAT	62	
Db	7_1198	TATGTCAGGTCTTACATGGAACTAAGTAACTGTTAGCAAGAACAT	62	
Qy	63	GGATTGCGATTGCTGGGAGCAGGGATTCCTATCCGCCCGTTAACGTGGAA	122	
Db	7_1138	GGACTCACATTAGTAGATGATGAGAATTAATCATCTCGATCATTACCGAAGGAA	71079	

Db	Qy	71078 TAACTTAACGGTGAATCAATAGAACATGCTACGGCGGATGGTTATTATCA 71019	AE017334_09	900001	1010000
Qy	183 ACTTGAAATATATATTGCGGAGGCATTATGAAAGCGGTATCTTGTGGCGCT	AE017334_10	100001	1110000	
Db	71018 TCAAGGAGGATCATATGGCGGAGGTAATAGCAGGATAGACATGTGCAACT	AE017334_11	110001	1210000	
Qy	243 TATTTCGGCTATCGGAGTACGAAACAGTACGGGAGAACCTACGGTCAAGTGT	AE017334_12	120001	1310000	
Db	70958 CTATTTCGGCTATCGGAGTACGAAACAGTACGGGAGAACCTACGGTCAAGTGT	AE017334_13	130001	1410000	
Qy	303 CCCGCGATGAGTTGAGCATGGTCTGTAGCTGCTGAGCTTGGAGAAGCTAAGA	AE017334_14	140001	1510000	
Db	70899 TCCATTGAGTTGAGCTTGTGAGCTGAGACAATCACTCTGTCAGAAGTTAAGA	AE017334_15	150001	1610000	
Qy	363 AAAGATTCGATCTTAACGATTTGAGAAAANTAGATCTATGGATACTAGTTTAC	AE017334_16	160001	1710000	
Db	70838 ATCTGTTAGATAGCATACCTTTTGATGATACCATATTACCGGATTAGACTTACCCACC	AE017334_17	170001	1810000	
Qy	423 GCTTCACTGATATGTCAGACGGACGGACGGACGGACGGACGGACGGACGGAGA	AE017334_18	180001	1910000	
Db	70778 ACTTACATGGATTAGCGGATAATGGGAGATGCTGATGCTGAGCTGAGCTGAGA	AE017334_19	190001	2010000	
Qy	483 CGGCCCTCAAAAGTCTATGATATCACCTGGTGTGAGACAGCCGACTTTATATG	AE017334_20	200001	2110000	
Db	70718 AGGATTAATTTGATGATGATGATGACCTAGAGCTAGAGGTGTGACGACATACCGGAGTTAAGA	AE017334_21	2100001	2210000	
Qy	543 GCATGTAACCAATCTGCAGCAATATACAGAACTGACGGAGGAGGAGGAGGAAAG	AE017334_22	2200001	2310000	
Db	70658 GCAATTACAATTTAGACAAATATATAGCCTTAATTCATGGCAGCATTGGCCACAGA	AE017334_23	2300001	2410000	
Qy	603 GATGGCGGATTACCCCTTCGTTTGCCAAAGGCTTAGGAAGCTGTTGGCTCGCCGGG	AE017334_24	2400001	2510000	
Db	70598 GTGCGGTAATTACCATTAAGTGTCTTGGCAAGGCTGGCTCAATGGACTTCAGG	AE017334_25	2500001	2610000	
Qy	663 GGAAATTACACCCCTTCGGGTTGAGAGCTGTTATTGAGAGAACATCTGAGSC	AE017334_26	2600001	2710000	
Db	70538 GGATTCAACCCGCCATCGAGGTTGTGGGGCGACGATGGCAAACACATCTGAG	AE017334_27	2700001	2810000	
Qy	723 GCGGGCGGATGAAAGGAAGGTCGACGCCGTTCAATTGGCAATATGAGGAT	AE017334_28	2800001	2910000	
Db	70478 TATAGATAGCGGAGAGAGGGATATCAGCCCTTTTCATATCTATCAATGAGG	AE017334_29	2900001	3010000	
Qy	783 ACCAAGGGCGCACTGATACGGGAGAGAGAACCTATATAAGCAATATCTCCGT	AE017334_30	3000001	3110000	
Db	70418 TCCTAAGGGTGGAGTAAACAGAGAAGGTGCTAGTAACTACATATACAGGT	AE017334_31	3100001	3210000	
Qy	843 GATGTGCAACGAAACTGAAACTACTATTCCACCACTAGACATCGCAAACTCAAA	AE017334_32	3200001	3310000	
Db	70358 AATGTTGATGGGATCCGGACACATATTATCATACATAGTGTGAGCAATTATAC	AE017334_33	3300001	3410000	
Qy	903 ACTAAATTATTCATGAGAGACTGACTGTTGGGCTTAAGTGTTCGGCTAAGC	AE017334_34	3400001	3510000	
Db	70298 TGTCTATTATTCATGAAATTAGATACAGAGGATTAAGCCTATCCGTCAAGC	AE017334_35	3500001	3610000	
Qy	963 AGAGAGGAGTATCAGACTTAAAGATCC 996	AE017334_36	3600001	3710000	
Db	70238 GAACACAAAAATATTATGAGAACTAAGTAGCC 70205	AE017334_37	3700001	3810000	
RESULT 8					
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WPCOMMENT					
Sequence split into 53 fragments LOCUS AE017334 Accession AE017334					
Fragment Name Begin End					
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AE017334_02	200001	310000			
AE017334_03	300001	410000			
AE017334_04	400001	510000			
AE017334_05	500001	610000			
AE017334_06	600001	710000			
AE017334_07	700001	810000			
AE017334_08	800001	910000			
Continuation 736 of 53) of AE017334 from base 3500001 (AE017334 Bacillus anthracis ssp. Anthracis)					
Query Match 29.4%; Score 293.2; DB 1; Length 110000;					
Best Local Similarity 55.9%; Pred. No. 1.9e-68; Mismatches 0; Mismatches 0; Conservativeness 43%; Indels 0; Gaps 0;					
Matches 556; Conservative 0; Mismatches 0; Conservativeness 43%; Indels 0; Gaps 0;					
Qy	3 TATGCGACAGCTACATGGAACTGCTGACCTAAAGTGTAGAGAACAT	70624 TATGCGACAGCTACATGGAACTGCTGACCTAAAGTGTAGAGAACAT	AE017334_52	5200001	5227419
Db	70564 GGACTTCACATTAGATATGATCAGAAGGATATAATCATCTCGACATTACAGTGGAA	70564 GGACTTCACATTAGATATGATCAGAAGGATATAATCATCTCGACATTACAGTGGAA	AE017334_53	5000001	5110000
Qy	123 CAGTGAGCTACGGGAGGCCCTAGACACAGTACAGCTGCGTTATGGTAGGGGAGAA	70504 TAATTAACGGTGAATCATTAATACAGAACATCTACGGTCAAGTGGATTATAC	AE017334_54	4900001	5010000
Db	70504 TAATTAACGGTGAATCATTAATACAGAACATCTACGGTCAAGTGGATTATAC	70504 TAATTAACGGTGAATCATTAATACAGAACATCTACGGTCAAGTGGATTATAC	AE017334_55	4800001	4910000
Qy	183 ACTTGAAATATATATTGCGGAGGCATTATGAAAGCGGTATCTTGTGGGGCT	70444 TCAAGGAGGATCATATTAGCGGGAGGAGTAATGAGCAGGATGACATGTGCAACT	AE017334_56	4700001	4800000
Db	70384 CTATTTCGGCTATGGGAGGCTGCTGAGCTGCTGAGCTTGTGAGAAGCTAAGA	70384 CTATTTCGGCTATGGGAGGCTGCTGAGCTGCTGAGCTTGTGAGAAGCTAAGA	AE017334_57	4600001	4700000
Qy	303 CCCGCGATGAGTTGAGCTGAGGAGGCTGCTGAGCTGCTGAGCTTGTGAGAAGCTAAGA	70324 TCCATTGAGTTGAGCTGAGGAGGCTGCTGAGCTGCTGAGCTTGTGAGAAGCTAAGA	AE017334_58	4500001	4610000
Db	70324 TCCATTGAGTTGAGCTGAGGAGGCTGCTGAGCTGCTGAGCTTGTGAGAAGCTAAGA	70324 TCCATTGAGTTGAGCTGAGGAGGCTGCTGAGCTGCTGAGCTTGTGAGAAGCTAAGA	AE017334_59	4400001	4510000

	REFERENCE
	AUTHORS
QY	363 AAAGATTCGATTTAACGATGTTAGAGAAGAAATTAGATCATTTGGATACAGTTTAC 422
Dp	70264 ATCTGCTAGATGCAATTACCTTGTGATATTACCGATTAGGACTTACGCCACC 70205
QY	423 GCTTCACTGGATATGTCAGGCCGAGGGCGGAACCTCGAGATAGAACAGAGCA 482
Dp	70204 ACTACATGGATTAGGGATAATGGGAGATGCAATTGTTAGGCT 70145
QY	483 CGGCCTCAAAGCTTGTGATATCAACCTGGTCTAGGAGACAGCCCGACTTATG 542
Dp	70144 AGGATTAATTTGTGATGAAACCTAGAGGAGGATGACGAACTTCCGGAGTTATG 70085
Qy	543 GCATCTAACCATCTGCAAGATATACAGATCAGGATGACGAGGATAGGACGAAAGA 602
Dp	70084 GCATTTACAAATTAGACATATAGGCCATTAAATGCCAGCATGGCCACAGA 70025
QY	603 GATGGCCGGATAGCCCTTCTGCTTGCACGGCTTGGAACTGTGTTGGCTCCGG 662
Dp	70024 GTGGGAGTAATTACCTTAAATGCCCTTTCAGGCTCAATGGACTTCCAGG 69965
QY	663 GATGATTATACCCGCCTCCCGTTGTCAGGCTGTTATTGAAAGAACATCTAGAGCC 722
Dp	69964 GGATTCACCCGCCATCGAGGTTTGCGGCCAGCATGGACAAACATTCAGAGG 69905
QY	723 GGCSCCGATGAAACGAAAGTGTACAGCGCTTTCACATTGCAATATGACGAT 782
Dp	69904 TATAGTAGAGGAGGAGGATATGCCCTTTCATCTTATGAGGT 69845
QY	783 ACCAAGGGCCAGTGTAAACGGAGAGGAAATTCACCATGACAATCGGAATCAA 902
Dp	69844 TCCTAAAGGTTGAGATAACAGAGAAGGGCATGATATGAGGT 69785
QY	843 GATGTCGCAACCAAATCTGAAACTACTATTCACCATGACAATCGGAATCAA 902
Dp	69784 ATGTTGATGGATTCGGACAAATATATCATCTAACGATGAGAACATTAGC 69725
QY	903 AGTAAATTATTCATGAGGAACTGACTGTTGAGTTTCGCTAAAGC 962
Dp	69724 TGTCTATTATTCATGAAATTAGATACAGATGAGTAAAGCTATCGGTCACG 69665
QY	963 AGAAGAGAGTTTCATGAGCTTAATTAAGGTC 996
Dp	69664 GAAACAAAAATTATTATGAGAACTAAGTAGGCC 69631
RESULT 9	
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LOCUS	AB017036
DEFINITION	291030 bp DNA linear BCT 01-MAY-2003
GENOME	Bacillus anthracis str. Ames section 13 of 18 of the complete genome.
ACCESSION	AB017036 AE016879
VERSION	AB017036_1 GI:30258352
KEYWORDS	
SOURCE	Bacillus anthracis str. Ames
ORGANISM	Bacillus; Firmicutes; Bacillales; Bacillaceae; Bacillus; Bacillus cereus group
REFERENCE	
AUTHORS	Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I., Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapfle, B., Okstad, O., Helgason, E., Rilstone, J., Wu, M., Kolonay, J., Beaman, M., Dodson, R., Brinkac, L., Gwinn, M., DeBoy, R., Madupu, R., Daugherty, S., Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H., Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J., Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A., Cline, R., Redmond, C., Twiss, J., White, O., Salzberg, S., Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and Fraser, C.
TITLE	The genome sequence of <i>Bacillus anthracis</i> Ames and comparison to closely related bacteria
JOURNAL	Nature 423 (6935), 81-86 (2003)
PUBLMED	12721629
REFERENCE	
	2 (bases 1 to 291030)
	Read, T., Peterson, S., Tourasse, N., Baillie, L., Paulsen, I., Nelson, K., Tettelin, H., Fouts, D., Eisen, J., Gill, S., Holtzapfle, B., Okstad, O., Helgason, E., Rilstone, J., Wu, M., Kolonay, J., Beaman, M., Durkin, A., Haft, D., Nelson, W., Peterson, J., Pop, M., Khouri, H., Radune, D., Benton, J., Mahamoud, Y., Jiang, L., Hance, I., Weidman, J., Berry, K., Plaut, R., Wolf, A., Watkins, K., Nierman, W., Hazen, A., Cline, R., Redmond, C., Twiss, J., White, O., Salzberg, S., Thomason, B., Friedlander, A., Koehler, T., Hanna, P., Kolsto, A.-B. and Fraser, C.
	Direct Submission
	Submitted (26-Mar-2003) The Institute for Genomic Research, 9712 Medical Center Dr, Rockville, MD 20850, USA
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 VERSION AL591975.1 AL591824 GI:16409709
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SOURCE Listeria monocytogenes
 ORGANISM Bacteria; Firmicutes; Bacillales; Listeriaceae; Listeria.
 REFERENCE Glaser, P., Frangeul, L., Buchrieser, C., Rusniok, C., Amend, A., Chakraborty, T., Baquero, F., Berche, P., Bloedel, R., Brandt, P., de Darvay, A., Dehoux, P., Chabot, A., Chetouani, P., Couve, E., de la Torre, A., Duran, L., Domann, E., Dominguez-Bernal, G., Duchaud, E., Durant, L.,

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 LOCUS Sequence 2855 from Patent WO0101118.
 DEFINITION AC041665.1 GI:28474426
 ACCESSION AX641665
 VERSION 1
 KEYWORDS
 SOURCE
 ORGANISM Listeria monocytogenes
 REFERENCE
 AUTHORS
 Buchrieser, C., Frangoul, L., Couve, E., Rusiok, C., Fehi, H.,
 Denouix, P., Dubusser, O., Chetouani, F., Nedjari, H., Glaser, P.,
 Kunz, F., Cobart, F., Daniel, B., J., Goebel, W., Kreft, J., Kuhn, M.,
 Ng, E., Vasquez-Boland, J., Dominguez, Bernal, G., Garrido-Garcia, P.,
 Tierrez-Martinez, A., Almend, A., Chakraborty, T., Domann, E., Hain, T.,
 Berche, P., Charbit, A., Durant, L., Perez-Diaz, J. C., Baguero, F.,
 Garcia del Portillo, F., Gomez-Lopez, N., Macueno, E., de Pablo, B.,
 Weiland, J., Kaest, U., Entian, K. D., Hauf, J., Rose, M. and Voss, H.,
 Listeria monocytogenes genome, polypeptides and uses
 TITLE
 JOURNAL
 Patent: WO 0101118-A 2855 11-APR-2001;
 INSTITUT PASTEUR (FR)
 FEATURES
 source 1. .349810
 /organism="Listeria monocytogenes"
 /mol_type="unassigned DNA"
 /db_xref="taxon:1639"
 /note="Seq 1 for big: original length: 2944528
 splitted into 10 <223>seq 001 : From 0.000.001 to 0.349.980 length: 349.980 <223>seq 2855 : From 0.300.001 to 0.649.980 length: 349.980 <223>seq 2856 : From 0.600.001 to 0.949.980 length: 349.980 <223>seq 2857 : From 0.900.001 to 1.249.980 length: 349.980 <223>seq 2858 : From 1.200.001 to 1.549.980 length: 349.980 <223>seq 2859 : From 1.500.001 to 1.849.980 length: 349.980

ORIGIN	Query Match	23.5%; Score 233.6; DB 6; Length 349980; Best Local Similarity 53.1%; Pred. No. 3e-52; Matches 497; Conservative 0; Mismatches 439; Indels 0; Gaps 0;	RESULT 15	Db	179620 TGTACTTGTGAGAGGTATAGAAATATCAA 179655
Qy	3 TATCTGCACAGTCATCTGAAACTCTGACCGTAAACATGTTAGCAAGACAT	62	LOCUS	AX413775	Sequence 766 from Patent WO0228891.
Db	178720 TAGTGACAGACGCTCAGCTGGATAGAACGTTAGATGAAACATTTATCAGACAT	178779	DEFINITION	AX413775	990 bp DNA linear
Qy	63 GGATTGTCATTCAGCTGGACAGAGGTATCTCATCCGCCGCGTACAGCTGCAA	122	VERSION	AX413775.1	PAT 02-SEP-2002
Db	178780 GGATTTGTCATTCAGCTGGACAGAGGTATCTCATCCGCCGCGTACAGCTGCAA	178839	SOURCE	Listeria monocytogenes EGD-e	REFERENCE
Qy	123 ATCTCTACAGACGGTGCATTAATTTATATAGATATGATTCATTTGTGGAGAA	182	AUTHORS	Kunst, F. and Glaser, P.	TITLE
Db	178840 ATCTCTACAGACGGTGCATTAATTTATATAGATATGATTCATTTGTGGAGAA	178899	JOURNAL	Listeria innocua, genome and applications	PATENT
Qy	183 ACTTGAGAATATAATTGCGAGGGCATTAATGAAAGGGTTATCTGTGGCCT	242	FEATURES	INSTITUT PASTEUR (I.P.R.) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (PR)	LOCATION/QUALIFIERS
Db	178900 GTTAGATANAAATACATTGCGAGGGATTGAAAGGGATTAGCTGIGACCT	178959	Source	1. .990	1. /organism="Listeria monocytogenes EGD-e"
Qy	243 TTTTTTCCGGCTATGGGGAGACGAAAAGATACTGGAGATACGGTCACATGT	302	/mol_type="unassigned DNA"		
Db	178960 ATATCTCCAGAGAACGCTTATGCCAACGACCTTAATCAATTAGC	179019	/db_xref="taxon:169963"		
Qy	303 CGCGCATGAGTTGACATGGCTCTGCTAGCTGTCACTCTTGGAGACCTAAAGA	362	Query Match	23.4%; Score 232.6; DB 6; Length 990; Best Local Similarity 53.0%; Pred. No. 6.1e-52; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;	RESULT 15
Db	179020 TCCACACAGATTTTGTCTTGTGCTGTTAGAACCTTGCCAACTTATCAGAACTG	179079	LOCUS	AX413775	Sequence 766 from Patent WO0228891.
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Qy	423 GCTTCACCTGGATATGTCAGACGGACCGGGAAACCTGACCAATAGACAGAGERA	482	SOURCE	Listeria monocytogenes EGD-e	REFERENCE
Db	179140 ATTACATGGATTTCAGACAGAGTGGCTGTGTTAGTGTACAGACAACTGAGAAC	179199	AUTHORS	Kunst, F. and Glaser, P.	TITLE
Qy	483 CGCCCTCAAAGCTATGATATCACCTGGTCATGAGAACGCCGACTTATG	542	JOURNAL	Listeria innocua, genome and applications	PATENT
Db	179200 ATCGCTCTGTATAAAGAAACCTGTGAGGTTATGACAATTAACGCCACGTGAA	179259	FEATURES	INSTITUT PASTEUR (I.P.R.) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (PR)	LOCATION/QUALIFIERS
Qy	543 GATGTTACCAATCTGCAAAATACAGGAATCAAGCAACAACTAGCGCAARGA	602	Source	1. .990	1. /organism="Listeria monocytogenes EGD-e"
Db	179260 GCTATCGAGAAATTACCAACTACACAGTTACAGCAACAACTAGCGCGTCAA	179319	/mol_type="unassigned DNA"		
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Db	179320 GTTGGAGAGTATGGCTAACATTGCGTAACTGCAAGGAAACCAATTACGG	179379	Query Match	23.4%; Score 232.6; DB 6; Length 990; Best Local Similarity 53.0%; Pred. No. 6.1e-52; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;	RESULT 15
Qy	663 GGTATATCACGGCTTCGGTTGTCAGACGTTTATGAAAGAACCTAGGCC	722	LOCUS	AX413775	Sequence 766 from Patent WO0228891.
Db	179380 TGCTTATCTCCGCCAGACGGTTGTCGCTGCGCATACCTGAAAGAAATTAAA	179439	DEFINITION	AX413775	990 bp DNA linear
Qy	723 GGGCGCATGATGAAAGGAGTAACTGGCGTTTAAATTGGAAATAGGAT	782	VERSION	AX413775.1	PAT 02-SEP-2002
Db	179440 AGCGAAAAACGAGAAGAGCTATCACAAATGGTGTGTTAGACGCTGCCC	179499	SOURCE	Listeria monocytogenes EGD-e	REFERENCE
Qy	783 ACCAAAGGGCGAGTGTAAAGAGAGGAATTCATGAACTTACGCAATATACCGT	842	AUTHORS	Kunst, F. and Glaser, P.	TITLE
Db	179500 TCGGAATGGAGGCTTAACTGAAAGTGTGACCTGTTACACGATCTGCACT	179559	JOURNAL	Listeria innocua, genome and applications	PATENT
Qy	843 GATGTCACAACTGAAACTACTATTCCACCATATGCAATGGCAATTCRCAA	902	FEATURES	INSTITUT PASTEUR (I.P.R.) ; CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE (CNRS) (PR)	LOCATION/QUALIFIERS
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Db	601 TCGGAGAGTATGGCTAACCATTTGCGAGGTTAGCGAGGTTAGCGAGG	660	/db_xref="taxon:169963"		

Qy	664	GATTATACACGCCCTCCCGGTTGTCAGACTGTATTGAAANGAACATCTAGGCCG	723
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Qy	724	CGGGCGATGAAACGAAAGGTAAACAGCCGTTCAATTGGAAATATGACGATA	783
Db	721	GCGAAAAAACGAGAAGAGCTATCACAAATGTCGTTGCTGAAACAGTCGGCATT	780
Qy	784	CCAAAGGGCGAGTGTAAACCGAAGAGACCSAATTCAATTACGCAATATGCACTTCGTC	843
Db	781	CGAAATGGAGGGTAAAGAAAGTGGTACCCCTGATTCAACAAATATGTCGATCT	840
Qy	844	ATGTCCAACGAACTGAAACTACTATTCACCATPATGCAATGGCAATCCAAAA	903
Db	841	ATGTGTTGGAAGCAAAACCTACTATTCACCTCATAGCAAAACACACAAATCATAGT	900
Qy	904	GTAATTATTCATGAGACCTTGACTGTGTTGGA	938
Db	901	GTTACTTGTGGAAGGAGTATGAAATAATGAA	935

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 Job time : 5418 sec

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Om nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:41:32 ; Search time 650 Seconds
(without alignments)

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Searched: 4996997 seqs, 3332346308 residues

Total number of hits satisfying chosen parameters: 9993994

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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14: geneseqn2005s;*

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	996	100.0	14 AEA39623	Aea39623 Bacillus
2	439.8	44.2	6 ABK74428	Abk74428 Bacillus
3	287.8	28.9	8 ACH21250	Aca21250 Prokaryot
4	23.8	9.9	8 ACA21947	Aca21947 Prokaryot
5	233.6	23.5	6 ABM03041_04	Continuation (5 of
6	232.6	23.4	6 ABG69869	Abg69869 Listeria
7	232.6	23.4	6 ABG67953	Abg67953 Listeria
8	232.6	23.4	8 AC33685	Aca33685 Prokaryot
9	196.4	19.7	13 ADR89833	Adr89833 Clostridi
10	177	17.8	6 ABM0521_18	Continuation (19 o
11	177	17.8	110000	Continuation (20 o
12	173.8	17.4	6 ABM0521_19	Acf15507 B spheaci
13	173.8	17.4	12 ADF57907	Adj62865 B spheaci
14	160.2	16.1	8 ACB46430	Aca46430 Prokaryot
15	159	16.0	4 AHS2150	Ahs2150 S. epider
16	159	16.0	6 ABM92958	Abm92958 Staphyloc
17	159	16.0	13 ADS02160	Ads02160 Staphyloc
18	159	16.0	4 AHS53981	Ahs53981 S. epider
19	16.0	4114	4 AHS54820	Ahs54820 S. epider

ALIGNMENTS

Result No.	Score	Query Match Length	DB ID	Description
1	996	100.0	14 AEA39623	RESULT 1
2	439.8	44.2	6 ABK74428	ID AEA39623 standard; DNA; 996 BP.
3	287.8	28.9	8 ACH21250	XX
4	23.8	9.9	8 ACA21947	AC AEA39623;
5	233.6	23.5	6 ABM03041_04	XX
6	232.6	23.4	6 ABG69869	DE 08-SEP-2005 (first entry)
7	232.6	23.4	6 ABG67953	DE Bacillus subtilis conjugated bile acid hydrolase gene, SEQ ID NO:1.
8	232.6	23.4	8 AC33685	XX
9	196.4	19.7	13 ADR89833	XX Plasmid; conjugated bile acid hydrolase; penicillin V acylase; chologlycine hydrolase; penicillin amidase; gene; ds.
10	177	17.8	6 ABM0521_18	XX
11	177	17.8	110000	XX Bacillus subtilis; NCIMB 11621.
12	173.8	17.4	6 ABM0521_19	XX
13	173.8	17.4	12 ADF57907	XX Key
14	160.2	16.1	8 ACB46430	XX Location/Qualifiers
15	159	16.0	4 AHS2150	XX CDS
16	159	16.0	6 ABM92958	XX FT
17	159	16.0	13 ADS02160	XX FT
18	159	16.0	4 AHS53981	XX FT
19	16.0	4114	4 AHS54820	XX FT

/tag= a /product= "Conjugated" bile acid hydrolase gene
/EC number= "3.5.1.24" /note= "Has penicillin V acylase (EC 3.5.1.11) activity"

WPI: 2005-457790/46.

New recombinant plasmid containing a chromosomal DNA fragment from Bacillus subtilis encoding conjugated bile acid hydrolase, useful for producing large amounts of Penicillin V acylase.

Claim 1; SEQ ID NO 1; spp; English.

XX
 CC The invention relates to a recombinant plasmid comprising a *Bacillus*
 CC *subtilis* NCIMB 11621 conjugated bile acid hydroxylase gene (CBH; AEAI9623)
 CC cloned between the BamHI and NdeI sites of pET-26b(+). The *Bacillus*
 CC (*EVA*, EC 3.5.1.11) activity, based on the presence of amino acid residues
 CC conserved between the hydroxylase and the putative active site of the
 CC solved structure of *Bacillus sphaericus* penicillin V acylase,
 CC V acylase catalyzes the hydrolytic removal of the phenoxycetic acid
 CC group of benzyloxy penicillin (pen V) to yield 6-aminopenicillanic acid
 CC (6-APA); an important precursor in the commercial production of semi-
 CC synthetic penicillins. The invention also relates to a recombinant strain
 CC of *Escherichia coli*, PTA 2456, comprising the plasmid of the invention;
 CC and a method for the recombinant production of the *Bacillus subtilis*
 CC conjugated bile acid hydroxylase/penicillin V acylase protein by
 CC fermentation using *Escherichia coli* PTA 2456. The plasmid, host cell and
 CC method are useful for the production of large quantities of conjugated
 CC bile acid hydroxylase/penicillin V acylase for use in the production of
 CC semi-synthetic penicillins. The present sequence represents the *Bacillus*
 CC *subtilis* NCIMB 11621 conjugated bile acid hydroxylase gene which encodes an
 CC enzyme having penicillin V acylase activity.

XX
 SQ Sequence 996 BP; 304 A; 198 C; 241 G; 253 T; 0 U; 0 Other;

Query Match 100.0%; Score 996; DB 14; Length 996;
 Best Local Similarity 100.0%; Pred. No. 7; 3e-307;
 Matches 996; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CATATGTCGCAAGCTTACATGTGGAAACTCTGTCGACCGTAACTGTTAGCAGAAC
 Db 1 ATGATTGTCGAACTTGAGCTTACATGTGGAAACTCTGTCGACCGTAACTGTTAGCAGAAC 60
 QY 61 ATGGATTGTCGATTCTAGCTGGAACTCTGTCGACCGTAACTGTTAGCAGAAC 120
 Db 61 ATGGATTGTCGATTCTAGCTGGAACTCTGTCGACCGTAACTGTTAGCAGAAC 120
 QY 121 AACAGTGAAATATATATATGCGCACGGCATTAATGAAGGGTTATCTGTGGGG 180
 Db 121 AACAGTGAACTGAGCTGAGGAAAGGCCATACAGAACAGTAGCGGTATGGGAGA 180
 QY 181 AACATGTTGAAATATATATGCGCACGGCATTAATGAAGGGTTATCTGTGGGG 240
 Db 181 AACATGTTGAAATATATATGCGCACGGCATTAATGAAGGGTTATCTGTGGGG 240
 QY 241 CTTATTTCGGGTATGGGAGTAGGAAAGATACGGGAGATACGGTTACATT 300
 Db 241 CTTATTTCGGGTATGGGAGTAGGAAAGATACGGGAGATACGGTTACATT 300
 QY 301 GTCCCCCATGTTGACTGGGCTCTGAGCTCTGGAGA 360
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 QY 361 GRAAAGATTCCGCTTAACTGATTTGAGAGAAAATTAGGCTCTTGGAAACCTTA 420
 Db 361 GRAAAGATTCCGCTTAACTGATTTGAGAGAAAATTAGGCTCTTGGAAACCTTA 420
 QY 481 CGCGCTCACTGATATGCGACGGCGAACCTGAGGAAAGCCGACTTAA 540
 Db 481 GACGGCCTCAAGTCATGATGATGATGCTGAGGAACTGGCGACTTAA 540
 QY 541 TGGCATGTAACATGCGACGAAATACGGGATCAGACGGGAGGAA 600
 Db 541 TGGCATGTAACATGCGACGAAATACGGGATCAGACGGGAGGAA 600
 QY 601 GAGATGGCGGATATTGCGCTTCTGCTTCCCAAGGCTTGGAACTGTTGGCTGCCG 660
 Db 601 GAGATGGCGGATATTGCGCTTCTGCTTGGAACTGTTGGCTGCCG 660
 QY 661 GGGGATTATAACCGCCTCCGGTTCTGAGGCTGTTTGTAAAGAACATCTAGAG 720

DB 661 GGCGGATTATAACCGCCTCCGGTTCTGAGGCTGTTTGTAAAGAACATCTAGAG 720
 ID 721 CGCGCGCGATGAAACGAAAGGTGAAACASCGCTTTCAATTGCGAAATATGCG 780
 ID 721 CGCGCGCGATGAAACGAAAGGTGAAACASCGCTTTCAATTGCGAAATATGCG 780
 QY 781 ATACCAAAGGGCCAGTGTAACTGAGGAGAGAATTCATATACCGCAATACTCC 840
 Db 781 ATACCAAAGGGCCAGTGTAACTGAGGAGAGAATTCATATACCGCAATACTCC 840
 QY 841 GTCATGTCGAACTGAGCTGGAAACTCTGTCGACCGTAACTGTTAGCAGAAC 900
 Db 841 GTCATGTCGAACTGAGCTGGAAACTCTGTCGACCGTAACTGTTAGCAGAAC 900
 QY 901 AAAGTAATTATTTCATGAGACCTTGACTGCTTGGCGCTTAAGTTTCCGCTAA 960
 Db 901 AAAGTAATTATTTCATGAGACCTTGACTGCTTGGCGCTTAAGTTTCCGCTAA 960
 QY 951 GCAGAGAGAGATTCTGAGCTTAATTAGGATCC 996
 Db 951 GCAGAGAGAGATTCTGAGCTTAATTAGGATCC 996

RESULT 2
 ABK74428
 ID ABK74428 standard; DNA; 990 BP.
 XX
 AC ABK74428;
 XX DT 13-AUG-2002 (first entry)
 XX Bacillus licheniformis genomic sequence tag (GST) #1719.
 KW Differential gene expression; genomic sequenced tag; GST;
 KW altered culture condition; environmental stress;
 KW physiological provocation; ds.
 OS Bacillus licheniformis.
 PN WO2002029113-A2.
 XX
 PD 11-APR-2002.
 XX
 PF 05-OCT-2001; 2001WO-US031437.
 XX PR 06-OCT-2000; 2000US-00580598.
 PR 27-MAR-2001; 2001US-0279526P.
 XX
 PA (NOVO) NOVOZYMES BIOTech INC.
 PA (NOVO) NOVOZYMES AS.
 XX
 PI Berka R, Clausen IG;
 XX
 WPI; 2002-416684/44.
 XX
 PT Monitoring differential expression of several genes in first *Bacillus*
 PT cell relative to expression of same genes in one or more second *Bacillus*
 PT cells, by using substrate containing *Bacillus* genomic sequenced tag
 PT array.
 XX
 PS Claim 4; SEQ ID NO 1719; 200pp; English.

XX
 The invention describes a method of monitoring differential expression of
 genes in a first *Bacillus* cell relative to expression of the genes in
 other *Bacillus* cells, comprising hybridising labelled nucleic acid probes
 isolated from *Bacillus* cells to a substrate containing array of *Bacillus*
 genomic sequenced tags (GST), examining the array, and determining
 relative gene expression by an observed hybridisation reporter signal of
 a spot in the array. The method is useful for measuring the expression of
 genes in a first *Bacillus* cell relative to expression of the same genes
 in one or more second *Bacillus* cell. The method is useful for monitoring
 global expression of several genes from a *Bacillus* cell, discovering new

genes, identifying possible functions of unknown open reading frames and monitoring gene copy number variation and stability. Monitoring changes in expression of genes may be used to provide a representation of the way in which *Bacillus* cells adapt to changes in culture conditions. Extensive follow environmental stress or other physiological provocation. Extensive follow -up characterisation is unnecessary, when one spot on an array equals one gene or one open reading frame, since sequence information is available. This sequence represents a genomic sequence tag (GST) used in the method of the invention. Note: The sequence data for this patient did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 990 BP; 247 A; 214 C; 285 G; 244 T; 0 U; 0 Other;
 Best Local Similarity 44.2%; Score 439.8; DB 6; length 990;
 Matches 645; Conservative 0; Mismatches 342; Indels 0; Gaps 0;
 QY 4 ATGTGACAGACTTACATGGAAACTCTGACCGTAACATGTTAGCAAGAACATG 63
 Db 1 ATGTGACAGATCACGTTGACGACTTGCGCCGGAGCATTTGGAGGAGATG 60
 QY 64 GATTTCATTCAGCCTGGGACAGAGGTGATCTCTACCGGGTTAACCTGGAC 123
 Db 61 GATTTCATTCAGCCTGGGACAGAGGTGATCTCTACCGGGTTAACCTGGAC 123
 QY 124 AGTGAAGTGACCGAAGGGCCATCAGACAACATACSGTTATCGGTATGGAGAAA 183
 Db 121 ACTGAACCGGACCGCAGGAGATGCCGCCCGTATGGTTATCGGTATGGAGAAA 180
 QY 184 CTGGAATAATATATTGCGACGGCATTAATGAAAGCGTTATCTGCGGGCCTT 243
 Db 181 CTCAGAATGCTCTCTGTTGCGAATGAAAGATGCTGCGGGCCTT 240
 QY 244 TATTTCGGGTATGGGAGTACGAAACACATACGGAGATACCGTTACATGTC 303
 Db 241 TATTTCGGGTATGGGAGTACGAAACACATACGGAGATACCGTTACATGTC 303
 QY 304 CCCATGAGTTGACATGAGGGTGTCAAGTGTCACTTGGAGACCTAAAGAA 363
 Db 301 CGCAGCAGATGTCGACTGGCTCGGAAATGGAGTCGGCGCG 360
 QY 364 AAGATTGATCTTAACGATCTAGAGAAATTAGATCTATTGGATACGTTCACG 423
 Db 361 GGCGCTGTTCTTAACTATGTTGAGAGAGGTCACTGCTGACTACGGCCG 420
 QY 424 CTCACAGGATTTGAGACGGACGGCGCGAACCTGACGATAGACAGACAGAC 483
 Db 421 CTGCAATTGGCTTAACGGACGGCTCGGGGAGACGCTCGTGTGACCGACAGAC 480
 QY 484 GGCTCAAAGCTATGATAATCACCTGGTCTCATGAGAACAGCCGACTTATGG 543
 Db 481 GGCACTCAATTGATGAACTGGCTCGGGTCTGAGAACAGTCGGATTCCTGG 540
 QY 544 CTGTAACCAATCTGCAGCAATTACAGGATCAGCGGAACTTAGAGACAGAACAG 603
 Db 541 CATTGACCAATTGGCAACTTATCGGTCTCAGCCGGACAGTTGCCGAAAAA 600
 QY 604 ATGGGGGATAGGCCCTTCGCTTGGCAGGCTAGAACCTGTTGGCTGGGG 663
 Db 601 ATGGGGCCTGACGCTCGCTGGTCTGAGGTTCGGCTGRCGATGGACAGGA 660
 QY 664 GATTACACGCCCTCCGGTTGAGCTGAGCTGTTATTGAAAGACATCTAGGCCG 723
 Db 661 GATTTAGCCGCAATCCGGCTTGGCTGAGGGTGCATTGAAAGACAGACGCT 720
 QY 724 CGGGCGATGAAAGAGGTGAACTACAGCCCTTCAAATTGGCAATTAGACGATA 783
 Db 721 GTGTCGATGAAAGAGGGCTCTGCCGGTTATGCTCTCCAAATGAAATT 780
 QY 784 CCAAGGGGAGGTGATAACCGAAGACAAATTCAATTAGCAATTACTTCGTG 843
 Db 781 CCTAAAGGGTGTGACTGATCAAGGCAAGACGATTACCCATAACGGCGTA 840

RESULT 3
 ID ACA21250 standard; DNA; 984 BP.
 XX AC ACA21250;
 XX DT 19-JUN-2003 (first entry)
 XX DE Prokaryotic essential gene #2907.
 XX KW Antisense; ds; prokaryotic essential gene; cell proliferation;
 KW drug design; gene.
 OS Bacillus anthracis.
 PN WO20027183-A2.
 XX PD 03-OCT-2002.
 XX PF 21-MAR-2002; 2002WO-US009107.
 PR 21-MAR-2001; 2001US-00815242.
 PR 06-SEP-2001; 2001US-0094893.
 PR 25-OCT-2001; 2001US-034223P.
 PR 08-FEB-2002; 2002US-00072851.
 PR 06-MAR-2002; 2002US-0362699P.
 XX PA (BLR-) ELTRA PHARM INC.
 XX PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KH, Zyskind JW;
 PT Wall D, Trawick JD, Carr GJ, Yamamoto R, Foreyth RA, Xu HH;
 XX DR WPI; 2003-029926/02.
 XX PS P-PSDB; ASU17380.
 XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.
 XX PS Claim 14; SEQ ID NO 9120; 176pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product; or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene

CC product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target polynucleotide essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp wipo.int/pub/published_pct; sequences

XX SQ Sequence 984 BP; 336 A; 165 C; 207 G; 276 T; 0 U; 0 Other;

Query Match 28.9%; Score 287.8; DB 8; Length 984;
Best Local Similarity 56.0%; Pred. No. 1.1e-80; Matches 544; Conservative 0; Mismatches 427; Indels 0; Gaps 0;

QY 4 ATGTGCACAACTCATCGAACATGCTGACCGTAACCTGTTAGCAAGAACATG
1 ATGTGCACAACTCATCGAACATGCTGACCGTAACCTGTTAGCAAGAACATG 63

Db 64 GATTTCGATTTCAGCTGGGACAGAGGTGTTCTATCGCGCGTAAAGCTGGAC 123

QY 61 GACTTCACATTTAGATGATGAACTGAGAAGTAAATGATTCCTCGACATTACAGTGAT 120

QY 124 ATGTGAAGCTGAGGGGCCATCAGACAACTGAGTACCGTTATCGTTATGGGGAAA 183

Db 121 ATATATACGGGTGAATCATTATACGAACATGCTACGGTGGAAATGGTTAAATCAT 180

QY 184 CTTGGAATAATATTATTTGACGGCATTTATGAAAGCGTTAACCTGGGGGGTT 243

Db 181 CRAGGAGGAGCATATTAGCG3ACGGGATATGAGCAGGGATAGCAACACTC 240

QY 244 TATTTCGGGCTATGGGGTAGCGAAAACGATACGGAGATAACCGTTACATGTC 303

Db 241 TATTTCAGGGATTCTGCTACTTTATGCAAGCATAGTAGACAAACACAAATTGGCT 300

QY 304 CGCGCATCTGTTGTGACATGCTGCTGCTCACTCTGTCAGTTTGGAGAGCTAAAGAA 363

Db 301 CGATTGATTGTGAACTTGTGACTCTGACACAACTCATCTGTCAGAGCTAAAGAA 360

QY 364 AGATTCGATCTTAAGATGTTAGAGAAATTAGATCATCTGATGTTACCG 423

Db 361 TGTGATGATAGCATTTTGATGATACCATCTGGATTAGACTTACGCCACCA 420

QY 424 CTTCACCTGGGATATGTCAGACGGGACGGCCGAACCTGACGATAGACAGAGAC 483

Db 421 CTACATTGGATTAGGGATAATGGGGATGATGCTGATGTTACTGGATCCGACAGTAA 480

QY 484 GGCCTCAAGCTCTATGATAATCACCTGGTGTGATGAGAACAGCCCGATTTAAGG 543

Db 481 GGATTAATATGATGATACCACTAGGATGATGAGAAATGGCTTAATGG 540

QY 544 CATGTAACTCATGCAATATAGCTTAATGCGAACATTAAGGCTTAATGG 603

Db 541 CATTACAAATTAGAACATATAGCTTAATGCGAACATTCGGCCACAGAG 600

QY 604 ATGGCCGGATAGCCCTTCTGCTTGGCAGGTTAGACTGTTGGTGGCGGG 663

Db 601 TGGAGTAATTACATTAGTGTCTTGGCTCAATGGACTCTCCAGGG 660

QY 664 GATTTACACCGCCTCCGGTTGTCAGAGCTGTTATTGAGAACATCTAGGCC 723

Db 661 GATTCACCCCGCATCGGTTGCGGGCAGCATGCAACAAACATCGGT 720

QY 724 GCGCCGATGAAAGAAGGTGTAACAGCGCTTCAATTGGCAATATGACGATA 783

Db 721 ATGATAGCGGAGAGGGAGTACGCCCTTCTCATCTTACATGAGGT 780

QY 784 CCAAAGGGCGACTGATAACGGAGAACAAATTCAATTACGCATAACTTCGTG 843

RESULT 4
AC21947 ID AC21947
XX ID AC21947 standard; DNA; 969 BP.
XX AC21947;
XX DT 19-JUN-2003 (first entry)
XX DR Prokaryotic essential gene #3604.
XX KW Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.
XX OS Bacillus anthracis.
XX WO200277183-A2.
XX PD 03-OCT-2002.
XX PP 21-MAR-2002; 2002WO-US009107.
XX PR 21-MAR-2001; 2001US-0081542.
XX PR 06-SEP-2001; 2001US-0094893.
PR 25-OCT-2001; 2001US-0342923P.
PR 08-FEB-2002; 2002US-0072851.
PR 06-MAR-2002; 2002US-0362699P.
XX PA (BLIT-) ELTRA PHARM INC.
XX PT Wang L, Zamudio C, Malone C, Baselbeck R, Ohlsen KL, Zyskind JW;
PT Wall D, Trawick JD, Carr GT, Yamamoto R, Forsyth RA, Xu HH;
XX DR WPI; 2003-029926/02.
XX P-PSDB; ABU18077.

New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids, required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

Claim 14; SEQ ID NO 9817; 176pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation or the biological identifying a gene required for cellular proliferation or its gene product lies pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an

organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than *S. aureus*, *S. typhimurium*, *K. pneumoniae* or *P. aeruginosa*. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp://wipo.int/pub/published_pct_sequences

XX
SQ Sequence 969 BP; 320 A; 175 C; 206 G; 268 T; 0 U; 0 Other;

Query Match 23.8%; Score 237; DB 8; Length 969;
Best Local Similarity 55.5%; Pred. No. 1.8e-64; Mismatches 425; Indels 6; Gaps 4;

Qy 4 ATGGCACAGTCATCGGAACTGTGACATTTACATGTTACCAAGAACATG 63
Db 1 ATGTTGACTAGTGTGACATTAGACAAACAAACGGTCGACATCTTGGAGATG 60
Qy 64 GATTGCGTTTCAGCTGGGACAGAGGTCTCTATCCGCCGTTACAGTGAC 123
Db 61 GACTTCACATTAAGTAGATGATCAGAAGAATGATAATCATCTCGACATAC 120
Qy 124 AGTGAAGCTACGGAAAGGCCCATGCAGACAGTCAGCGCTTATCGGATGGAA 183
Db 121 AATATAACGGTGAATCATTAATAGACAAACATGCTACGGTCGGATGGTTATCAT 180
Qy 184 CTTGAAATATATTGCGGGCATTAAGAACGGTTATCTTGCGGGCTT 243
Db 181 CAAGGAAGCATCTATGGGACGGGAAATGAGCAGTCAGCTGGAGAA 240
Qy 244 TATTTCGGCTATGGGAGTACGAAACACGATACGGAGATACGGTACATGTC 303
Db 241 TATTTCGAGGATTCGACTTAATGTCAGAACATAGATGACACACAGGATTGCT 300
Qy 304 CGCGATGAGTTGACATGGGCTGTCGTCATGCTGCTGCTT-GGAGAGCTAAAG 361
Db 301 CCATTGATTGTAATGACTGGAGTCGACAACTCAITCTGCAAGAGCCAGTGAGA 360
Qy 362 AAAGATTGCGATCUTTAAGGATGTTAGAGAAAATTGATCTATTGGATA-AGTTTA 420
Db 361 AATCTGTAGATGACATTACCTTTGGATAATCATTACCGCATTTAGACCTAC 420
Qy 421 CGCTTCACTGATGTCAGACGGAGGGCGAACCTGAGATAGACCAAGAGCA 480
Db 421 CGCTTCACTGATGTCAGACGGAGGGCGAACCTGAGATAGACCAAGAGCA 480
Qy 481 GACGGCCCTCAAGCTCTGTCATGAACTCTGGTCAAGACAGCCGACTTAA 540
Db 481 GAGGGATTAAATGTGATGATTAACCACTAGGGATGATGCGATAGTCGGATTAT 540
Qy 541 TGGATGAACTATGCGCATATACGAAATCAGACGAGCAATTAGAGAAA 600
Db 541 TGGATGAACTATGCGCATATACGAAATCAGACGAGCAATTAGAGAAA 600
Qy 601 GAGATGGCGGATAGCCCTTCGCTTGGCAAGGGCTAGGAATCTGGTCTCGG 660
Db 601 GAGTGGGATATTACCTTGGGAGCTGGCTTGGCAAGGGCTAGGAATCTGGTCTCGG 660
Qy 661 GGGGATGATCACCCTGGCATTCGAGGTTGCGGAGCATGGCAACACATCAA 720
Db 661 GGGGATGATCACCCTGGCATTCGAGGTTGCGGAGCATGGCAACACATCAA 720
Qy 721 CGGGCGCCGATGAAACGAAAGSTGTAACAGGGCTTTCMAATTGGCAATATGAGC 780
Db 721 GGTATAGATAGCCGAGAAGGGAGTACAGCCTTTATCATCATGATGTGAG 780

RESULT 5
ABA03041_04

Continuation (5 of 30) of ABA03041 from base 40001 (*Listeria monocytogenes* EGD-e gen)

WP	Sequence	Contamination	Fragment Name	Begin	End
WP	ABA03041_00	1		110000	
WP	ABA03041_01	100001		210000	
WP	ABA03041_02	200001		310000	
WP	ABA03041_03	300001		410000	
WP	ABA03041_04	400001		510000	
WP	ABA03041_05	500001		610000	
WP	ABA03041_06	600001		710000	
WP	ABA03041_07	700001		810000	
WP	ABA03041_08	800001		910000	
WP	ABA03041_09	900001		1010000	
WP	ABA03041_10	1000001		1110000	
WP	ABA03041_11	1100001		1210000	
WP	ABA03041_12	1200001		1310000	
WP	ABA03041_13	1300001		1410000	
WP	ABA03041_14	1400001		1510000	
WP	ABA03041_15	1500001		1610000	
WP	ABA03041_16	1600001		1710000	
WP	ABA03041_17	1700001		1810000	
WP	ABA03041_18	1800001		1910000	
WP	ABA03041_19	1900001		2010000	
WP	ABA03041_20	2000001		2110000	
WP	ABA03041_21	2100001		2210000	
WP	ABA03041_22	2200001		2310000	
WP	ABA03041_23	2300001		2410000	
WP	ABA03041_24	2400001		2510000	
WP	ABA03041_25	2500001		2610000	
WP	ABA03041_26	2600001		2710000	
WP	ABA03041_27	2700001		2810000	
WP	ABA03041_28	2800001		2910000	
WP	ABA03041_29	2900001		294528	

Query Match 23.5%; Score 233.6; DB 6; Length 110000;
Best Local Similarity 53.1%; Pred. No. 2.7e-62; Mismatches 439; Indels 0; Gaps 0;

Qy 3 TATGCGACAGCTTCATGGATGAACTCTGGCTACCGTAACTGTTAGCGAGCAT 62
Db 78720 TATGCGACAGCTTCATGGATGAACTCTGGCTACCGTAACTGTTAGCGAGCAT 78779
Qy 63 GATTTGCGATTCAGTGGGGACAGGGGTGTTCTATCCGGCGGTACAGCTGAA 122
Db 78780 GATTTGCTTATTGAGGGCAACAACTAGCCAAAGAATTGGATGGATGAA 78839
Qy 123 CAGTGGCTACGGAGGGCCATGACAGACAGCTGGCTTGGGAGAA 182
Db 78840 ATCTCTACAGAGGGCTTAAATTATAGATGATGCTTGGGGAGAGA 78899
Qy 183 ACTTGGAAATATTTGGCGGCAATGAGGGTTATCTTGCGCGCT 242
Db 78900 GTTAGATAATCATTTGCGGAGGATGACGCGATGAGGATGAGCTCT 78959

QY	243 TATTTTCCGGCTATGGGAGTACGAAAAAACGATAACCGAGATAACCGTCATCT	XX	(INSP) INST PASTEUR.
Db	78960 ATATCTTCCAGGAGAGCAGTTATGCCGCAGCACCGAGAAATCAATTAGC	XX	(CNRS) CNRS CENT NAT. RECH SCI.
QY	303 CCCGGATGAGTTGGACATGGGCTCTGTCAGTCGTCAGTTGGAGAGCAGTAAGA	XX	DR
Db	79020 TCCACAAAGATTTCGGCTTGCTTGCTTGAGACTTGCGCAGATTAAGATGGAGC	XX	WPI: 2002-332479/37.
QY	363 AAAGATTCGATCTTAAACGATGTGAGAGAAATTAGTCATATGGATACAGTTAC	XX	New genomic sequences from Listeria species, useful for detection, treatment and prevention of infection, also related polypeptides, PT antibodies and modulators.
Db	79080 AAAGATTCGATCTTAAACGATGTGAGATCAACGATACCGTACCTACTGGATCACAC	XX	PT
QY	423 GCTTCACTGCTATATGTCAGACCGAGCGAGCGAAACCTGACGATGAGAACAGA	XX	PR
Db	79140 ATTGCACTGGATTTCACAGCAAGGAGCTGGTGTAGTGTGAACCAACAGAAC	XX	PR
QY	483 CGGGCTCAANGCTATGATATCAACCTGGTGTGATGACGACGCCGACTTATG	XX	PS
Db	79200 ATCGCTTCTGATTAAGAAACCCCTGAGGTATGACAAATGCCACGGATGAAAC	XX	Claim 16; SEQ ID NO 2682; 180pp; French.
QY	543 GATGTAACCATCTGGAGCAATACAGGATCAGACGGAGCAATTAGAGGAAAGA	XX	The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g., as contaminants in foods, or mutational analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WPO at ftp.wipo.int/pub/published_pct_sequences . (Updated on 29-AUG-2003 to standardise OS field)
Db	79260 GCATATCGAGAAATTAGCAGACTAACAGGTTAACAGCACACATTAGGCCGGTGA	XX	CC
QY	603 GATGGCGGAGTAGCCCTTGCTGTTGGCAAGCTTAGGAACTGGACAGCTGGGG	XX	CC
Db	79320 GTTCGGAGAGTATATGCTAACATTTCAGGAGAACAGAACATTACAGG	XX	CC
QY	663 GGATTTACACGCCGCTTCGGGTTGAGCTGTTATTGAAAGAACATCTAGAGC	XX	CC
Db	79380 TGGTATATCTCGCCAGACCGTTGGCGGATCTGGAGAAATTATAAA	XX	CC
QY	723 GCGGGCGATGAAACGAAAGGTATCACAAAGCTTCAGGGCTTCAATTGGAAATATGAGAT	XX	CC
Db	79440 AGCAGAAAACCAAAGAGAAGGTATCACAAAGCTGGTAACTCGCTTCAATTGGAAATATGAGAT	XX	CC
QY	783 ACCAANGGGCCAGTGATAACCGAGAAGAGAAATTCTATTACCGAATTAACCTCCG	XX	CC
Db	79500 TCGGAATGGAGCGGTAAATTAGAAAGTGGTACCTGTGATTTCACAAATGTCAT	XX	CC
QY	843 GATGTCGCAACCAAACCTGGAACATACGTTACCACTATCACAACTGGCAATTCAAA	XX	CC
Db	79560 TAGTGTGTCGGAAGCAGCAACGTACTTACCTATCACAAACACCAATCATAG	XX	CC
QY	903 AGTAATTATTATCATGAGACCTGACTGTTGAA 938	XX	CC
Db	79620 TGTACTTTGGCAAGGAAAGTTAGAAATTATGAA 79655	XX	CC
RESULT 6	ABQ6869 ABQ6869 Standard; DNA; 990 BP.	XX	Sequence 990 BP; 347 A; 171 C; 215 G; 257 T; 0 U; 0 Other;
ID	ABQ6869;	XX	Query Match 23.4%; Score 232.6; DB 6; Length 990;
AC	ABQ6869;	XX	Best Local Similarity 53.0%; Pred. No. 4; -7e-63; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;
XX	29-AUG-2003 (revised)	XX	Matches 1 ATGGCAAGCTCTGTTAGAGGTTAGATGAGGATTCAGTTCAGTCATG 63
DT	29-AUG-2002 (first entry)	XX	4 ATGTCACAGTCTACATTGGAACCTGCGCTAACATGATTAGCAAGAACATG 60
XX	Listeria monocytogenes EGDe DNA sequence #81.	XX	1 ATGGCAAGCTCTGTTAGAGGTTAGATGAGGATTCAGTTCAGTCATG 60
DE	Antibacterial; Listeria; food contamination; mutational analysis; infection; ds.	XX	64 GATTGTCATTCAGCTGGGAGAGGATGTTCTTCGCGCCGTRACAGCTGGAC 123
KW		DB	61 GATTGTCATTCAGCTGGGAGAGGATGTTCTTCGCGCCGTRACAGCTGGAC 120
OS		XX	124 ATGGAGCTGGGGAGGCCATAGACAGACAGACGGTTATGGTATGGGAA 183
XX		DB	121 TCTTCATACAGGGGCCATATTAGATGATGATTGCTTGTGAGGGAGAGG 180
XX		XX	184 CTTCGAAATATATTATTTGGGAGCGGATTAATGAGGGCTTATCTTGCGCGCT 243
XX		DB	181 TTGATAATAACATTCTGGAGACGGATGATGAGGATGAGGATGCTGCACTTA 240
XX		XX	244 TATTTCGGCTATGGGAGGAAACGATACGGAGATACCGTTGAGGAAATCAATTAGCT 303
XX		DB	241 TATCTTCAGGGAGGAGGATTAATGAGGGATGAGGATGAGGATGCTGCACTTA 300
XX		XX	304 CGGGATGAGTTGGACATGGTGTGTCGTCGTCGTCGTCGTCGTCAGTTGGAGA 363
XX		DB	301 CCACAGAAATTTCGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 360
XX		XX	364 AAAGATTCGATCTTAAACGATGTGAGAGAAATTAGATCTTGGATGAGGATGAGGAGC 423
XX		DB	361 AGTATTCGATCTTAAACGATGTGAGAGAAATTAGATCTTGGATGAGGATGAGGAGC 420
XX		XX	424 CTTCAGCTGGATGGACGGGGCGAAACCTGAGATGAGGAGGAGGAGGAGC 483
XX		DB	421 TTAACCTGGATTCAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGC 480
XX		XX	484 GGCTCAACGCTTGTAACTCAACCTGGGTGTCAGGAGACAGCCGACTTTATGG 543
XX		DB	481 TCGCTTGATTAAGAAACCTGAGGATTTACGAAATACGCCACCGCATCGATGG 540
XX		XX	544 CATGAAACCTGGACGAACTACGAGGTTACAGGAGAACAGAACAAATTAGGGGGAG 603
XX		DB	541 CATACGGGTTGGCAACTACGAGGTTACAGGAGAACAGAACAAATTAGGGGGAG 600
PR	04-OCT-2001; 2001WO-FR003061.	XX	
	04-OCT-2000; 2000FR-00012697.	XX	

CC on 29-AUG-2003 to standardise OS field)

XX Sequence 990 BP; 347 A; 215 C; 257 T; 0 U; 0 Other;

SQ Query Match Best Local Similarity 23.4%; Score 232.6; DB 6; Length 990; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

Db 604 ATGGCGGATATTAGCCCTTTCGCTTTGGCCAAAGCCTTAGGAACTGTGTCCTGCCGGG 663
601 TTGGAGAGTATATGGCTAACCATTTCCGAAGTGACGAAACAGCAATTACCGT 660

QY 664 GATTAATCACCGCCCTCCGGTTTCAGGGCTTATTGAGAGACATCTAGAGCG 723
661 GGTTATACCTCCGCAGAACCTTTCGGCGGCATACTTGAAAGAAATTTAATAA 720

Db 724 GCGGCCGATTAACCAAAGGGTACAGGGCTTCAAGTGGCAAAATGAGATA 783
721 GCGAAAMACGAGAGAGACTTACAAATGTCGTTGAGACAGTGCCGTT 780

QY 784 CCAGAGGGCCAGTGTAAACGGAAGAGACAAATTCTTACGCAATATCTTCGG 843
781 CGGATGGAGCGGTTAAGAGAGTGGTACCTGTGTTTACACATATGGCATCT 840

QY 844 ATGGCACACGAACTGGAACTATATTTCACCACTATGACATGGCAATCCAAA 903
841 ATGTTGCGGAAGCAAAAGTACATTACCTTACCTCATCGAAACCAATCAATG 900

QY 904 GTAAATTATTCTGAGAGCTGACTCTTGA 938
901 GTTACTTGTGAGGAGTTATGAAATATGAA 935

RESULT 7

ABQ67953 ID ABQ67953 standard; DNA; 990 BP.

XX AC ABQ67953; DT 29-AUG-2003 (revised)
XX 29-AUG-2002 (first entry)

DB Listeria monocytogenes EGD DNA sequence #77.

XX KW Antibacterial; listeria; food contamination; mutational analysis;
KW infection; db.

OS Listeria monocytogenes; EGD.

XX PN WO200228891-A2.

DD 11-APR-2002.

PP 04-OCT-2001; 2001WO-FR003061.

PR 04-OCT-2000; 2000FR-00012697.

XX PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.

XX PI Kunst F, Glaser P;

XX DR WPI; 2002-332479/37.

XX PS Claim 16; SEQ ID NO 766; 180pp; French.

The present invention relates to nucleic acid sequences (ABQ67188-ABQ71212) from Listeria sp. The sequences are useful as probes and primers for identification and/or detection of Listeria (e.g. as contaminants in foods, or nutritional analysis) and for analysis of gene expression. Proteins encoded by the nucleic acid sequences can be used to screen for compounds that modulate gene expression, replication and pathogenicity of Listeria (potential therapeutic agents), also for treating infections by Listeria and are useful as immunogens in anti-Listeria vaccines. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences. (Updated

CC 244 TATTTCGGCTATGGGAGTACGAAAAAGATAGGGAGATACGGTCACATGTC 303
Db 241 TAATCTTCAGGAGAGCAGTGTATGCCAGCACCAGTGGAAAGAAATCAATTAGCT 300

QY 304 CGGCGATCTAGTTGAGATGGTGTCTGCTGAGTCTTGAACTTGCCAACTTAAGAA 363
Db 301 CCACGACGATTTTGCTTGGTGGAACTTGCCAACTTAAGAAATGGAAAGCA 360

QY 364 AAGATGGATCTTAAAGATGTTAGAGAAATAATTAGATCTTGGTACAGTTAACCG 423
Db 361 AAGTATGGTTAAACTTGTTGAACTGGTCAACCGTACCGTTGGAATCAACCCA 420

QY 424 CTTCACGGATATGGTACGGGACGGAAACCTGAGATAGGACCAAGAGCAGAC 483
Db 421 TTAAGCTGGATTTCACAGACAGTGGTGGCTTGTGTTAGTGGATACCTTACCG 480

QY 484 GCCTCAAGCTATGTTAACCTGGTCTGGTACGGACAGCCCGACTTATTTGG 543
Db 481 TCGCTTGTTAAAGAAACCTGGGAGTATGACAATACGCAACGATTCGATGG 540

QY 544 CAGTAACCAATCTGCGCAATACGGAAATCAGCGAACTAGGCAAAAGAG 603
Db 541 CATACTCGAAATTACCGCAACTACAGCTGGTTAACCGAACAACTAGGCCGGTCAAG 600

QY 604 ATGGCGGATATTAGCCCTTTCGCTTTGGCCAAAGCTTGGCTTGCGGGG 663
Db 601 TTGGAGAGTATATGGCTAACCATTTTCGCAAGGTACAGGAAACAAATTACCGT 660

QY 664 GATTATCACCCCTCCGGTTGGTACAGCTGGTTATTGAAAGACATCTAGAGCG 723
Db 661 GGTTATACCTGCCAACAGCTGGTGGCGCTTCAATTGGCAAAATATGACCA 720

QY 724 GCGGCCGATGAAACGAGAGGTTAAGCAGCCCTTCAATTGGCAAAATATGACCA 783
Db 721 GCGAAAMACGAGAGAGACTTACAAATGTCGTTGAGACAGTGCCGATT 780

QY 784 CCAGAGGGCCAGTGTAAACGGAAGAGACAAATTCTTACGCAATACTTCGG 843
Db 781 CGGATGGAGCGGTTAAGAGAGTGGTACCTGTGTTTACACATATGGCATCT 840

QY 844 ATGGCACACGAACTGGAACTATTTACCACTATGACATGGTCGTTGAGAC 903
Db 841 ATGTTGCGGAAGCAAGTACATTACCTCATCGAAACCAACAAATCAATG 900

QY 904 GTAAATTATTCTGAGAGCTGACTCTTGA 938
Db 901 GTTACTTGTGAGGAGTTATGAAATATGAA 935

Query Match Similarity Score DB Length
Best Local 50.8% 196.4; 13; 1087;

RESULT 10

Qy Matches 501; Conservative 0; Mismatches 486; Indels 3; Gaps 3 TATGTCACAGTCTTACATGGAAACTGCTGAGCCGTAACATGTTATTGCAAGAACAT 62

Continuation (19 of 24) of ABA90521 from
WP Sequence split into 24 fragments LOCUS
WP Fragment Name Begin End
WP ABA90521 00 1 11000

QY	241	CTTATTTCGGGATGCGGAGTACGGAAACGATACGGAAATACGGTCACATT	300	PD
Db	3822	TGTATTCCAGGCTATGCTGACTATAGTAGAATCAAAAGGAAATT	3763	PP
QY	301	GRCGGCATGATGTTGACATGGGCTGCTGAGTCAGTCAGTCAGTCAGTAA	360	XX
Db	3762	TCACTTGATGATGTTATCCACGCGCTACTCAGTCAGCGACTTA	3703	PA
QY	361	GAAGAGATCGATCTAACGTTAGAGAAAATTAGCTA--TUGGATACAGTT	417	PT
Db	3702	GATTATTGATAAAAATTGTTATTTCTGTTAGTAAATGTAATGACTAATCCACCTAGGTCTACG	3643	XX
QY	478	GCAGGGCTCAAGTCTATGATAATCACCTGGGTGAGACACGCCCTT	537	PT
Db	3582	CAAGGGACTTCAATTAAAGATCATTGAGGTGAGAATAGTCRATTAC	3523	PT
QY	538	ATATGCTATGTAACCAATCTCAGGATATACAGGATCAGACCGAACCTAGGAGC	597	PT
Db	3522	CAATGCGACCAACTTATTAAGATAATTATCTTACCTATCAAAGGAACT	3463	PT
QY	598	AAAGGATGGGGATTAGCCCTTCTGCTTGCACAGCTTGGAACTGTTGCTCTG	657	PT
Db	3462	ATCGAACTTATAGGAAAGACATAAAACCTTACGGTCAAGTCAGTCTTGGATT	3403	PT
QY	658	CCGGGGATTATACCCGCCCTCCGGTTGTCAGCTTATTGAGAACATCA	717	PT
Db	3402	CCAGGAGATTTACCTCTCAAGATTGTTACACGGCTTAAACTACAGCT	3343	PT
QY	718	GASCGCGCGCCGATGAAAGCTGTCACAGCGCTTCAATTGGCAATAG	777	PT
Db	3342	GAGAACCAAGTAATGAAATTAGCCCTTACGGCTTGTCACTCATATAAGAATCTGA	3283	PT
QY	778	ACGTTACCAAGGGCCAGTGTAAAGGAAGAGCGAAATCATATAAGCAATACT	837	PS
Db	3282	ATTATCCAAAGGAAATTGTATACCTGACATGCGAAGTGTACTTGTATCG	3223	XX
QY	838	TCCGTATGTCACGAAACTGGAAACTACTATTCACCACTATGACATCGGAAATC	897	CC
Db	3222	GCATATGCTGCTGAGAACTCTAGTTCACTTGGTATCAAGAATC	3163	CC
QY	898	CAAAAGTAATTATTCTGAGACCTTGACTGTTGGAGCTAACGTTTCCGCT	957	CC
Db	3162	AGGAAATAATGTTGTCAGATCTGTAAATGAGAAGGAAATTAAACTTCTATT	3103	CC
QY	958	AAAGCAGAGAGACTATCTGAGCTTAATTA	990	CC
Db	3102	GTCATATGAGGAGATTTAGCTTAATG	3070	CC
RESULT 12				
ACF57507				13-NOV-2003.
ID	ACF57507	standard; DNA; 1616 BP.		
XX				
AC	ACF57507;			
DT	22-APR-2004 (first entry)			
XX				
DE				
XX				
B	sphaericus penicillin-V-amidase DNA SEQ ID NO: 8.			
KW	protein targeting; angiogenesis inhibitor; fusion gene; cancer; gene; ds;			
KW	antiangiogenic; cytotoxic; ophthalmological; antiarrhythmic;			
KW	antirheumatic; antiinflammatory; dermatological; immunosuppressive;			
KW	antiparasitic; antidiabetic; neuroprotective; vasotropic; anorectic.			
OS	Bacillus sphaericus.			
XX				
PN	WO2003093303-A1.			

Qy

481 GACCGCCCTGAAAGTCATGATAATCACCTGGTCATCAGAACAGCCCCGACTTTATA 540

Db

815 A CAGGCATTACCATCATTGAAAGAAGATGCGTCATGACGAATAGCCCTGGCTTGTGAA 874

Qy

541 TGGCATGAACTACAACTCTGCGCAATACAGGATCGACGGAGAACATAGGAGCAA 600

Db

875 TGGCATGAACTACAACTCTGCGCAATACAGGATCGACGGAGAACATAGGAGCAA 934

Qy

601 GAGATGGGGGGGATTAAGCCCTTCTCGCTTGGCCAGGTTAGGAACTGTTGGCTGGG 660

Db

935 ATGATGGGGAGCTGGATGACACGGTTGGCGAGGTTAGGAACTGTTGGCTGGG 994

Db

661 GGGGATTAACCGCCCTCCCGTTGTCAGAGCTTACATGGTGTCACCCAAATCGGCCA 720

Qy

995 GGAGATGGGGGGGATTAAGCCCTTCTCGCTTGGCCAGGTTAGGAACTGTTGGCTGGG 1054

Db

721 CGCGGGGGGATGAAACGAGGGTAACGGCGCTTCAAAATTGCAATATGAGG 780

Qy

1055 AACGCCAAATATGAAACAGAGGCTAACACTGTTCTCGGGTAGCATCTGAA 1114

Db

781 ATACCAAAGGGGGAGTAACTGGAGAGGAAATCTTACGGAGAACTTACGGATAACTCC 840

Qy

1115 ATCCCAAAGGGGGATGAAACGAGGTTATACCTCTTACCTCTAACCTCA 1174

Db

841 GTGATGTCACGAAACTGAAACTACTATTCCACCACTATGACATCGCAATCCAA 900

Qy

1175 GCTATGTCACGAACTGAAACTACTATTCAACTGATGAACTGTTGAACTGAA 1234

Db

901 AAAGTAATTTATTCATGAGAACCTTGACTGTTGAGCTTGTGAACTGTTGAA 960

Qy

1235 GCGGTTCCCTTAATGCTGAAATTAAATAGTCAGATTAACTACATTTGAGGGAT 1294

Db

961 GCAGAGAGAGGATTCATGAGCTTAATTAGGA 993

Qy

1295 CGTAACACAAGTATTAAATCAAGTA 1327

RESULT 13
ADT62865 ID ADT62865 standard; DNA; 1616 BP.

AC

XX ADT62865;

DT

06-MAY-2004 (first entry)

XX B sphaericus penicillin-V-amidase gene related to cancer treatment.

DE

XX beta-catenin; bipartite T-cell factor; Tcf; promoter construct; Lef-1; cytostatic; beta-catenin activity inhibitor; gene therapy; colon cancer; metastasis; liver; thymidine kinase; prodrug; chemotherapy; radiation therapy; surgery; penicillin-V-amidase; gene; ds.

OS

Bacillus sphaericus.

XX

US2003228285-A1.

PD

11-DEC-2003.

XX

05-MAY-2003; 2003US-00429802.

PP

03-MAY-2002; 2002US-0377672P.

XX

(HUNG/) HUNG M.

PA

(KWON/) KWONG K Y.

PA

(ZOU/) ZOU Y.

PT

Novel viral vector comprising beta-catenin/bipartite T-cell factor-

responsive promoter having first and second promoter region linked to

target nucleic acid sequence, useful for treating colon cancer.

Disclosure; SEQ ID NO 17; 114pp; English.

PX

RS

This invention relates to a novel viral vector comprising a beta-catenin/bipartite T-cell factor (Tcf)-responsive promoter construct which contains a first promoter region having a copy of Tcf/Lef-1 binding site operatively linked to a second promoter region, and a nucleic acid sequence, where the first and second promoter regions are operatively linked to target nucleic acid sequence. The invention may be useful for the development of compounds with a cytostatic activity, through action as betta-catenin activity inhibitors, or for gene therapy. The invention may be useful for treating an individual with colon cancer which is metastasised to the liver. The treatment involves administering the vector of the invention where the nucleic acid sequence encodes a therapeutic polypeptide or thymidine kinase, a prodrug and chemotherapy, radiation, surgery or gene therapy to the individual. The present sequence is that of a therapeutic gene which may be used in the vector of the invention for the treatment of an individual with cancer.

CC

QY 721 CCGGGGCGCATGAAACGAAAGGTGACAGCGCTTCAATTGGAAATNGACC 780
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 Db 1055 AAAGCCAAATGAGAACAGGCGTAACCTGTTCTATTCCTCTGTAAT 1114
 QY 781 ATACCAAAGGCCGCGATGAAACGGAGAGAACGAAATTATAACGGCATATCTC 840
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 Db 1115 ATCCCAAAGGCGTGTGTTGACAATGAGGGAAACGGATAACCTATACCTA 1174
 QY 841 GTGATGTGCGACGAACACTGAAACTATGTTCCACACTATGACAAATGGCAATCC 900
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 Db 1175 GCTATGTCGACAGTAAACTATCTTAAACTGTATGACAAATGTCGATTC 1234
 QY 901 AAGCTTAATTATTCATGAGACCTTGACTGTGTTGGACCTAAGTGTTCGCTAA 960
 CC |||||
 CC |||||
 CC |||||
 CC |||||
 Db 1235 GCGGTTCCCTAATGCTGAATTTAAATAGTCAGATTAACTATGAGTGGAT 1294
 QY 961 GCAGAGAGAGTATGAGCTTAAATTAGGA 993
 CC |||||
 CC |||||
 Db 1295 CGTAACAGATTAAGGAAATTAATCAGTA 1327

RESULT 14

SQ ACMA46430

ID ACMA46430 standard; DNA; 978 BP.

XX XX

AC ACMA46430;

XX XX

DT 19-JUN-2003 (first entry)

XX DE Prokaryotic essential gene #28087.

XX KW Antisense; ds; prokaryotic essential gene; cell proliferation; drug design; gene.

XX OS Staphylococcus epidermidis.

XX PN WO200277183-A2.

PD 03-OCT-2002.

XX PR 21-MAR-2002; 200240-US009107.

PR 21-MAR-2001; 2001US-00815242.

PR 25-OCT-2001; 2001US-0094933.

PR 08-FEB-2002; 2002US-00072851.

PR 06-MAR-2002; 2002US-0362699P.

XX PA (BLT-) ELITRA PHARM INC.

PI Wang L, Zamudio C, Malone C, Haselbeck R, Ohlsen KL, Zyskind JW, Wall D, Trawick JD, Carr GJ, Yamamoto R, Forsyth RA, Xu HH; DR DR

DR P-PSDB; ABU42560.

XX PT New antisense nucleic acids, useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs.

PS Claim 14; SEQ ID NO 34300; 1766pp; English.

The invention relates to an isolated nucleic acid comprising any one of the 6213 antisense sequences given in the specification where expression of the nucleic acid inhibits proliferation of a cell. Also included are: (1) a vector comprising a promoter operably linked to the nucleic acid encoding a polypeptide whose expression is inhibited by the antisense nucleic acid; (2) a host cell containing the vector; (3) an isolated polypeptide or its fragment whose expression is inhibited by the antisense nucleic acid; (4) an antibody capable of specifically binding the polypeptide; (5) producing the polypeptide; (6) inhibiting cellular proliferation or the activity of a gene in an operon required for

CC proliferation; (7) identifying a compound that influences the activity of the gene product or that has an activity against a biological pathway required for proliferation, or that inhibits cellular proliferation; (8) identifying a gene required for cellular proliferation or the biological pathway in which a proliferation-required gene or its gene product lies or a gene on which the test compound that inhibits proliferation of an organism acts; (9) manufacturing an antibiotic; (10) profiling a compound's activity; (11) a culture comprising strains in which the gene product is overexpressed or underexpressed; (12) determining the extent to which each of the strains is present in a culture or collection of strains; or (13) identifying the target of a compound that inhibits the proliferation of an organism. The antisense nucleic acids are useful for identifying proteins or screening for homologous nucleic acids required for cellular proliferation to isolate candidate molecules for rational drug discovery programs, or for screening homologous nucleic acids required for proliferation in cells other than S. aureus, S. typhimurium, K. pneumoniae or P. aeruginosa. The present sequence is one of the target prokaryotic essential genes. Note: The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX SQ Sequence 978 BP; 357 A; 152 C; 158 G; 311 T; 0 U; 0 Other;

Query Match 16.1%; Score 160.2; DB 8; Length 978;
 Best Local Similarity 49.9%; Pred. No. 6.1e-40; Indels 6; Gaps 2;
 Matches 458; Conservative 0; Mismatches 453; InDel 6; Gaps 2;

QY 4 ATGTCGACAGCTTACATGGAAACTCTGACCGTAAACATGTTATGGCAAGAACATG 63
 Db 1 ATGCGTAGGCTTACATGGAAACTCTGACCGTAAACATGTTATGGCAAGAACATG 60
 QY 64 GATTTCGATTTCAGCTGGGACAGAGCTGGATCTCTATCCGGCCCTACAGCTGGAC 123
 Db 61 GACTTGCATTGATTAATGGTATCCACCATTTCCACGTCATATCACCC 120
 QY 124 ATGGAAAGTGACCGGAAGGCCATCACAGACAGTACCGTTATCGGATATGGGAGAAA 183
 Db 121 TTGATCTAGATCA--GACATGCGCTTGATATGTTGCAACAATTAA 177
 QY 184 CTGGAAATATATTATGGCGACGGATTATGAAAGGGTTATTTGTGGCGCTT 243
 Db 178 GTAGGACTTATGATGTTGATGTTAAGCAGAAAGGTATTAGTTTGAACT 237
 QY 244 TATTTCCGGCTATGGGAGTACGAAAAACGATACGGGAGATACGGTCACTTC 303
 Db 238 TACTCTGTTGAACTCATACGACCCATAAGTATGGTTTAACTGCA 297
 QY 304 CCCATCGTGTGACATGGGGTGCTCAGCTGTGTTAGCTTGGAGACGTAAGAA 363
 Db 298 CCTGAGGAGTTATGTTGGGTTAATTAAGTATTAGGAATTAACAA 357
 QY 364 AGATGGATCTTAAGATGTTAGGAAAMATTAGCATATTGATACGTTCC 423
 Db 358 AAGGTTAGAGATCAATTATGAAAGAAATACAACTTGTGATATCGTCTCCT 417
 QY 424 CTCACTGGATATGACGGACGGCGAACCTGACGATAGGACGAACTTATATGG 483
 Db 418 TTAATCTGTTGATGAACTGATGAAACGACATACCTGACGACTACATGG 477
 QY 484 GGCTCTAAGTCATGAACTGCGCAATATCGGATCTGACGACGCGGACTTTATGG 543
 Db 478 TTAATCTGTTGATGAACTGATGAAACGACATACCTGACGACTACATGG 537
 QY 544 CATGTCACGCTTACGCTGCGCAATATCGGATCTGACGACGCGGACTTTATGG 603
 Db 538 CAGCTACTCTAATGAACTGATGTTACACGACGAAATCACCATA 597
 QY 604 ATGGCCGATAGCCCTTCCTTGGCAAGCTTGGACTGTTGGCTGGGGGG 663
 Db 598 ATAGGTAAGCTGTTAGGATCAATGGGTTGAGCAGACAAATGGCTACGGGT 657
 QY 664 GATTATCACCGCTTCGGGTTGGAGACATCTAGAGCCG 723

Db 658 GGTATCTTAACTGAAAGCTTATACGGCTACATTTAACACATACGGCTT 717
 Qy 724 GCGGCCGATGAAACGAAGGTGAAACGGCTTCATAATTGGCAATATGAGATA 783
 Db 718 TCCATAATGAGAATTATTAGATTGTTTAAGTCTAGANTCAGTCAGTTC 777
 Qy 784 CCAAAGGGCGACTATAACGGAAAGACGAATTCAATTAGCAATATCTCCGTC 843
 Db 778 CCTCAAGGTCAGTAT--CGATGCCATAAAATCATACATCACACAATATCAATTAGTG 834
 Qy 844 ATGTCGAACTGGAACACTATTCACCTATGACAACTGGAAATCCAAA 903
 Db 835 ATGGAAGTAAAGAAAGACTTATTAAGCCATACCTTAGTAATCAATTTCATAA 894
 Qy 904 GAAATTATTTCATGA 920
 Db 895 ATAAATTAACTGAGA 911

RESULT 15

AAH52510 AAH52510 standard; DNA; 990 BP.
 AC AAH52510;
 XX DT 03-SEP-2001 (first entry)
 DE S. epidermidis open reading frame nucleotide sequence SEQ ID NO:413.
 XX KW Staphylococcus epidermidis SR1 strain; infection; diagnosis; vaccination;
 XX endocarditis; ds.
 OS Staphylococcus epidermidis.
 XX PN WO200134809-A2.
 XX PD 17-MAY-2001.
 XX PF 09-NOV-2000; 2000WO-US030782.
 PR 09-NOV-1999; 99US-0164258P.
 XX PA (GLAXO) GLAXO GROUP LTD.
 PT Kimerly WJ;
 XX DR WPI: 2001-31495/33.
 DR P-PSDB; AAG81660.
 XX PT Nucleic acids encoding polypeptides from Staphylococcus epidermidis,
 XX useful for vaccinating against infections, e.g. endocarditis.
 PS Claim 8; Page 151-152; 2188pp; English.
 XX
 CC AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG81120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cell which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH33971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA poly nucleotide sequences from the present invention. AAH55091 to AAH55098 represent oligonucleotide sequences and primers which are used in the exemplification of the present invention. N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464

CC Sequence 990 BP; 361 A; 158 C; 158 G; 313 T; 0 U; 0 Other;

XX

Query Match Score 159; DB 4; Length 990;
 Best Local Similarity 16.0%; Pred. No. 1 5e-39;
 Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Db 2 ATATGTGCGAACTGCTTACATGGAACCTGCTGACCTPAACGTATAGCAAGAAA 61
 Qy 62 TGGATTTGCATTCTGAGGGACAGGGTGTCTATCGGGCGTTACGCGA 121
 Db 68 TGGACTTCTGATTGAAATTAGGTATCCAAACATTGTTGTCACGCCATTACACC 127
 Qy 122 ACAGTGAGCTGAGGGGGCCATCAGACACAGTGCGGTTATCGGAGAAA 181
 Db 128 AATTGTAATCTAGATTCAGACATCGGTCTT--GATATGGTTGTTGAGAACATTAA 184
 Qy 182 AACATGGAGCTATATTAGATTCAGACSCATTATGAGAACAGGGAGATACCGT 241
 Db 185 AACATGGAGCTATATTAGATTCAGACSCATTATGAGAACAGGGAGATACCGT 244
 Qy 242 TTATTTCCGGCTATCGGGAGTACGAAAAACGATTCGGAGATGGGGAGATTCACATG 301
 Db 245 ATRACTTCACTGAGAACTCATACGTTACCCATAACGTTATGGTTATTAACTAG 304
 Qy 302 TCCCGCATGAGTTGTCATGGTGTCACTGCTGAGCTTGTGAGCTTAAAG 361
 Db 305 CACCTGAGGAGTTATGTTGGGTITAGTTTAATTAAGTATTTGGGAAAC 364
 Qy 362 AAGAGATGATCCTTAACGATGTTGAGAAMAAATGATCTATTGCTACAGTTAC 421
 Db 365 AAAAGGTTAGAAATCATATTAGTAAGAAGAAATACGACTTGTGATATGCTTC 424
 Qy 422 CGCTTCACTGGAATTCGACAGCGAGGGCGAACCTGAGCATGAGTACGAGAG 481
 Db 425 CTTTACATTCTGCTCTGCTGAAAGAACAGGAACTACCGTASCATACACCTCACATG 484
 Qy 482 ACGGCCTCAAGCTATATACTACCTGGGTTGAGGAAATGAGCTTACCTTAC 541
 Db 485 GCTTATTAGTAGTAAGAAATAATGTTCTACCTTACAGGAACTGAGCCGACTTAT 544
 Qy 542 GGCGATGTTACCAATCTGAGCAATATACTAGGAACTGAGCGAACATAGAGCAAG 601
 Db 545 GGCGATCTCAACTTAAGAAATTACGTTTAACTGAGGAACTACCATCAT 604
 Qy 602 AGATGGCGGATGAGCCCTTCCTTGGCGCAGGGTTAGGACTCTGGCTGCGG 661
 Db 605 TAATGTTAGTCAGTCTGAGATCAATGGCTGTAAGCAGGAACTACGCTTACCCG 664
 Qy 662 GGGATTAACCCCTTCCCGGTGTCAGGGTTGAGGTATTTGAGGAACTAGAC 721
 Db 665 GTGGTTATACGTCACAGAACTCGTTTACGGCTACATATTAGACACCACTACGT 724
 Qy 722 CGGGGCCATGAAACGAAGGGTAAAGCCCTTTCATAATTGCGAAATATGAGA 781
 Db 725 GTTCCCATATGAGATAAAATTATGAACTTGTGAGCTTACGATCTGAGTCAGTCA 784
 Qy 782 TACCAAGGGCGAGTGTACGGAGAGACAAATTCTGAGGAACTATCTCCG 841
 Db 785 TCCCTCAAGTGTGAGTAT--CCATGCAATAAAATCATACACACATATCATAG 841
 Qy 842 TGTGTGAGCAAGAACTGAACTACTTCCACCATAGACATGCGAAATCCA 901
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 Qy 902 AAGTAAATTTCATGA 920
 Db 902 AAATAATTAACTGAGA 920

Mon Mar 20 10:09:57 2006

us-10-812-387-1.rng

Page 15

Search completed: March 18, 2006, 12:55:34
Job time : 654 secs

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OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:46:51 : Search time 4766 Seconds
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.					
SUMMARIES					
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C 1	85.8	8 6	595	9 BH861030	BH861030 297 Liste
C 2	45.2	4 5	853	10 C2540175	C2540175 SRAA-aad3
C 3	44.6	4 5	175	9 CY973894	DDP370 Br
C 4	44.6	4 5	881	9 A2533653	A2533653 ENTICS2TR
C 5	44.6	4 5	910	9 A253681	A253681 ENTFFH6TP
C 6	44.6	4 5	910	9 BH155642	BH155642 ENTSS6TR
C 7	41.4	4 2	842	9 A2688508	A2688508 ENTFL24TR
C 8	41.4	4 2	871	9 A2683787	A2683787 ENTKU4TF
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C 12	38.6	3 9	1101	10 CN500100	AL070854 Drosophil
C 13	38.2	3 8	575	11 CR008507	CR008507 Forward 6
C 14	38.2	3 8	593	3 B0266623	B0266623 NISC ff14
C 15	38.2	3 8	853	9 A266993	A266993 ENTIPD0TP
C 16	38.2	3 8	859	9 A2691994	A2691994 ENTJUN3TF
C 17	38.2	3 8	881	9 A2546452	A2546452 ENTFP8TR
C 18	38.2	3 8	918	9 A268664	A268664 ENTIP6TF
C 19	38.2	3 8	929	9 BH149784	BH149784 ENTQD8TF
C 20	38.2	3 8	286	2 BH12826	BH12826 1029P1P
C 21	38.2	3 8	534	9 BH4273	BH4273 g178C09.b
C 22	38.2	3 8	632	2 BB661316	BB661316 ORIGIN

ALIGNMENTS

Query Match	8.6%	Score	85.8	DB	9	Length	595	
Best Local Similarity	54.6%	Pred.	No. 6-6-14					(P.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk)
Matches	171	Conservative	0	Mismatches	142	Indels	0	at the University of Bristol, Bristol, UK. Sequencing by Washington University Genome
QY	626	CTTGTGGCCAAAGGCTTAGGAACTCTGGCTGGCGGGGSGATATAACCGCCTTCGGT	685					Sequencing Center, St. Louis, MO."
Db	590	CATTTCGCAGAGGTACAGGAACAAGCAATTACAGGTGTATCTCGCCAGAACGTT	531					
QY	686	TGTGAGGTGTTCAATTGCGCAATTAGGACATCTAGGCCGGCATGAAAGCAAGTG	745					
Db	530	TGTGCGCCGCAACTTGAAAGAAATATATAAACGGAAAACGAGAAGAAGCT	471					
QY	746	TAACAGGCCCTTCAATTGCGCAATTAGGACATCTAGGCCGGCATGAAAGCAAGTG	805					
Db	470	TCAAGATGTGGTAGTGTCTGAAACAGTGCTCCGATTCGGAATGGAGGGTAATTAAAG	411					
QY	805	AAGAGACGAAATCATTAGGACATATCTGGATCTGTGAACTGAACT	895					
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QY	926	TGACTGTTGGA	938					
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RESULT 2								
LOCUS	CZ540175	853 bp	DNA	linear	GSS	13-MAY-2005		
DEFINITION	SRA0-ad30b09.b1	Strongyloides ratti whole genome shotgun library						
ACCESSION	(SRAGSS 004)	Strongyloides ratti genomic, genomic survey sequence.						
VERSION	CZ540175.1	GI:64664074						
SOURCE	GSST							
ORGANISM	Strongyloides ratti							
REFERENCE	1	(bases 1 to 853)						
AUTHORS	Mitreva,M., McCarter,J.P., Thompson,F., Viney,M., Pape,D., Mitterer,B., Martin,J., Wylie,T., Dante,M., Waterston,R.H., Clifton,S.W. and Wilson,R.							
TITLE	Genome Survey sequences from the rat parasitic nematode Strongyloides ratti (unpublished (2005))							
JOURNAL	COMMENT							
CONTACT	Mitreva M							
Washington University in St. Louis								
Washington University School of Medicine								
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA								
TEL:	314 286 1800							
FAX:	314 286 1810							
Email:	nematode@watson.wustl.edu							
Genomic DNA was provided by Fiona Thompson (F.Thompson@bristol.ac.uk) and Mark Viney (Mark.Viney@bristol.ac.uk) at the University of Bristol, Bristol, UK.								
Class: shotgun.								
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FEATURES	source							
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/de stage="seven days after infection with Peronospora								
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FEATURES	source							
1.	526	Location/Qualifiers						
/organism="Brassica oleracea"								
/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
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/clone_lib="Brassica oleracea DD-PCR fragment"								
FEATURES	source							
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/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
/de stage="seven days after infection with Peronospora								
/clone_lib="Brassica oleracea DD-PCR fragment"								
FEATURES	source							
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/organism="Brassica oleracea"								
/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
/de stage="seven days after infection with Peronospora								
/clone_lib="Brassica oleracea DD-PCR fragment"								
FEATURES	source							
1.	526	Location/Qualifiers						
/organism="Brassica oleracea"								
/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
/de stage="seven days after infection with Peronospora								
/clone_lib="Brassica oleracea DD-PCR fragment"								
FEATURES	source							
1.	526	Location/Qualifiers						
/organism="Brassica oleracea"								
/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
/de stage="seven days after infection with Peronospora								
/clone_lib="Brassica oleracea DD-PCR fragment"								
FEATURES	source							
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/organism="Brassica oleracea"								
/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
/de stage="seven days after infection with Peronospora								
/clone_lib="Brassica oleracea DD-PCR fragment"								
FEATURES	source							
1.	526	Location/Qualifiers						
/organism="Brassica oleracea"								
/cultivar="CRG3.1"								
'Algarvia' and 'Coracao-de-Boi'								
/de stage="seven days after infection with Peronospora								
/clone_lib="Brassica oleracea DD-PCR fragment"</td								

RESULT 4	
LOCUS	AZ533653/c
DEFINITION	ENTC832TR Entamoeba histolytica Sheared genomic, genomic survey sequence.
ACCESSION	AZ533653
VERSION	AZ533653.1 GI:11089512
KEYWORDS	GSS.
SOURCE	Entamoeba histolytica
ORGANISM	Entamoeba histolytica
AUTHORS	Bukaryota; Entamoebidae; Entamoeba.
TITLE	Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
JOURNAL	Unpublished (2000)
COMMENT	Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library	
Seq primer: M13-Reverse	
Class: shotgun	
High quality sequence start: 21	
High quality sequence stop: 842.	
FEATURES	Location/Qualifiers
Source	
1. . 881 /organism="Entamoeba histolytica" /mol-type="Genomic DNA" /strain="HMI:IMSS"	
/clone lib="Entamoeba histolytica Sheared DNA" /note="Vector: phosI; Site I; Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of <i>E. histolytica</i> using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. <i>Exp. Parasitol.</i> 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."	
ORIGIN	
Query Match 4.5%; Score 44.6; DB 9; Length 881; Best Local Similarity 49.8%; Pred. No. 0.15; Matches 113; Conservative 0; Mismatches 114; Indels 0; Gaps 0;	
383 TTGTAGAGAAATAGATCTATTGATCACTCGTTAACGGCTTCAGTGGATATTCAG 442	
632 TGTATAGACAATAATTCACAGTAGAATCATCTACTATCTGTATTAATATAA 573	
443 ACCGGACGGCGAACCTGAGATGAGAACGAGACGCCGACTTATGGATGACCAATCTGCAG 502	
572 ATCACAAATGAGAACATGACATATGGCTATACATGGAGAATATAGAAA 513	
503 ATCACCTGGTCTGAGAACAGCCCGACTTATGGATGACCAATCTGCAGC 562	
512 ATACATGGAAATATCAATATAAAACCCATGAGAACATGGCTCCATATAAGA 453	
RESULT 5	
LOCUS	AZ538681/c
DEFINITION	ENTC86CF Entamoeba histolytica Sheared genomic, genomic survey sequence.
ACCESSION	AZ538681
VERSION	AZ538681.1 GI:1143851
KEYWORDS	GSS.
SOURCE	Entamoeba histolytica
ORGANISM	Entamoeba histolytica
AUTHORS	1 (bases 1 to 910) Loftus,B., Van Aken,S. and Fraser,C.
TITLE	Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
JOURNAL	Unpublished (2000)
COMMENT	Contact: Brendan J Loftus Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0208 Fax: 301 838 3543 Email: bjloftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library	
Seq primer: M13-Forward	
Class: shotgun	
High quality sequence start: 50	
High quality sequence stop: 716.	
FEATURES	Location/Qualifiers
Source	
1. . 910 /organism="Entamoeba histolytica" /mol-type="Genomic DNA" /strain="HMI:IMSS"	
/db xref="taxon:5759" /clone lib="Entamoeba histolytica Sheared DNA" /note="Vector: phosI; Site I; Bst I; Constructed at The Institute for Genomic Research (TIGR), Rockville, MD. Genomic DNA isolated from broth cultures of <i>E. histolytica</i> using a method described by Clark and Diamond (Clark, C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a method for isolate identification. <i>Exp. Parasitol.</i> 77:450.). The DNA was mechanically sheared to give a tight size distribution (~2 kb). The v + i method used for the library construction is described in detail in Smith, H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In Genome Sequencing: A Practical Approach, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999)."	
ORIGIN	
Query Match 4.5%; Score 44.6; DB 9; Length 910; Best Local Similarity 49.8%; Pred. No. 0.15; Matches 113; Conservative 0; Mismatches 114; Indels 0; Gaps 0;	
383 TTGTAGAGAAATAGATCTATTGATCACTCGTTAACGGCTTCAGTGGATATTCAG 442	
370 TGTATAGACAATAATTCACAGTAGAATCATCTACTATCTGTATTAATATAA 311	
443 ACCGGACGGCGAACCTGAGATGAGAACGAGACGCCGACTTATGGATGACCAATCTGCAG 502	
310 ATCACAAATGAGAACATGACATATGGCTATACATGGAGAATATAGAAA 251	
503 ATCACCTGGTCTGAGAACAGCCCGACTTATGGATGACCAATCTGCAGC 562	
250 ATACATGGAAATATCAATATAAAACCCATGAGAACATGGCTCCATATAAGA 191	

Db	190	CATTAACATGATAATTGACATACAATAATGCATAAAGTGTGGAC	144	Db	407	CATTACATGATAATTGACATACAATAATGCATAAAGTGTGGAC	453
RESULT	6			RESULT	7		
BH155642	BH155642	923 bp	DNA	AZ688508/c	842 bp	DNA	linear GSS 14-DEC-2000
LOCUS	ENTSS56TR	Entamoeba histolytica Sheared DNA	Entamoeba histolytica	LOCUS	AZ688508	ENTSS47TR	Entamoeba histolytica Sheared DNA
DEFINITION	genomic, genomic survey sequence.			DEFINITION	AZ688508	genomic, genomic survey sequence.	
ACCESSION	BH155642			ACCESSION	AZ688508		
KEYWORDS	BH155642.1	GI:1527707		KEYWORDS	AZ688508.1	GI:11825654	
SOURCE	GSS.			SOURCE	GSS.		
ORGANISM	Entamoeba histolytica			ORGANISM	Entamoeba histolytica		
AUTHORS	Bukaryota; Entamoebidae; Entamoeba.			AUTHORS	Bukaryota; Entamoebidae; Entamoeba.		
TITLE	1 (bases 1 to 923)			TITLE	1 (bases 1 to 842)		
JOURNAL	HMI:IMSS Sheared DNA library (2001)			JOURNAL	HMI:IMSS Sheared DNA library		
COMMENT	Unpublished (2001)			COMMENT	Unpublished (2000)		
Department of Eukaryotic Genomics				Department of Eukaryotic Genomics			
The Institute for Genomic Research				The Institute for Genomic Research			
9712 Medical Center Dr., Rockville, MD 20850, USA				9712 Medical Center Dr., Rockville, MD 20850, USA			
Tel: 301 838 0208				Tel: 301 838 0208			
Fax: 301 838 3543				Fax: 301 838 3543			
Email: bjlloftus@tigr.org				Email: bjlloftus@tigr.org			
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library				Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library			
Seq primer: M13-Reverse				Seq primer: M13-Reverse			
Class: Shotgun				Class: shotgun			
High quality sequence start: 16				High quality sequence start: 45			
High quality sequence stop: 815.				High quality sequence stop: 609.			
FEATURES	source			FEATURES	source		
ORGIGIN	/organism="Entamoeba histolytica"			ORGIGIN	/organism="Entamoeba histolytica"		
Query Match	4.5%	Score 44.6; DB 9; Length 923;		Query Match	4.2%	Score 41.4; DB 9; Length 842;	
Best Local Similarity	49.8%	Pred. No. 0.15;		Best Local Similarity	48.9%	Pred. No. 1.3;	
Matches	113;	Conservative 0; Mismatches 114; Indels 0; Gaps 0;		Matches	111;	Conservative 0; Mismatches 116; Indels 0; Gaps 0;	
QY	383	TGTAGAGAAATTAGTCATTTACGGCTTCACTGGTATGGTCACTTGCG	442	QY	383	TGTAGAGAAATTAGTCATTTACGGCTTCACTGGTATGGTCACTTGCG	442
Db	227	TGTATAGCAAAATCATCACAGTAGATACTCTACTCTGTTATCAATA	286	Db	317	TGTAGAGAAATTAGTCATTTACGGCTTCACTGGTATGGTCACTTGCG	258
QY	443	ACCGGAGGGCGAACCTGCGATGACCCAGAGCAGGGCTCAAGCTATGATA	502	QY	443	ACCGGAGGGCGAACCTGCGATGACCCAGAGCAGGGCTCAAGCTATGATA	502
Db	287	ATCACAAATGAGAAACATGCAATTGGGAAATTGAGGAAATTAGAGAA	346	Db	257	ATCACAAATGAGAAACATGCAATTGGGAAATTGAGGAAATTAGAGAA	198
QY	503	ATCAACCTGGTGTAGCGAGACGCCGACTTATGGCATGAAACATCTGCAGC	562	QY	503	ATCAACCTGGTGTAGCGAGACGCCGACTTATGGCATGAAACATCTGCAGC	562
Db	347	ATACATGGAATAATCAATTAACACCCATATGAAACAACTTCCGATATAAGA	406	Db	197	ATACATGGAATAATCAATTAACACCCATATGAAACAACTTCCGATATAAGA	138
QY	563	ATATACAGGATCACCGAGCAATTAGAGCAAGAGATGGC	609	QY	563	ATATACAGGATCACCGAGCAATTAGAGCAAGAGATGGC	609
Db	137	CATCACATGATATTAAACAAATAATGCATAAAGTGTGAC	91	Db	137	CATCACATGATATTAAACAAATAATGCATAAAGTGTGAC	91

RESULT 8
AZ683787-C
Locus AZ683787
Definition Entamoeba histolytica Sheared DNA GSS 14-DEC-2000
Accession AZ683787
Version AZ683787.1 GI:11820933
Source GSS
Keywords
Organism Entamoeba histolytica
Entamoeba histolytica
Eukaryota; Entamoebidae; Entamoeba.
(bases 1 to 871)
Loftus, B., Van Aken, S. and Fraser, C.
Determination of clone end sequences from Entamoeba histolytica
HM1:IMSS sheared DNA library
Unpublished (2000)
Contact: Brendan J Loftus
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0208
Fax: 301 838 3543
Email: bjlloftus@tigr.org
Clones are derived from the Entamoeba histolytica HM1:IMSS sheared DNA library
Seq printer: M13-Forward
Class: shotgun
High quality sequence start: 25
High quality sequence stop: 860.
Location/Qualifier
Source
FEATURES
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/strain="HM1:IMSS"
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pGEM; Site I: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD."
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.). The DNA was mechanically sheared to give a
tight size distribution (~2 kb). The V + I method used for
the library construction is described in detail in Smith,
H.O. and Venter, J.C. (Making small insert libraries for
whole genome shotgun sequencing projects. In Genome
Sequencing: A Practical Approach, eds. M. Vaudin and B.
Barell, Oxford University Press, 1999)."
ORIGIN

Query Match Best local Similarity 4.2%; Score 41.4; DB 9; Length 871; Matches 111; Conservative 0; Pred. No. 1.3; Mismatches 116; Indels 0; Gaps 0;

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QY 383 TTGTGAGGAGAAAATTAGATCTATTGATACAGTTAACGGCTTACTGGATATTTGTCAG 442
Db 500 TTGTGAGGAGAAAATTAGATCTATTGATACAGTTAACGGCTTACTGGATATTTGTCAGAAAAA 441
Db 443 ACCGGCGGGCGAACCTGAGGATGAAAGCAAGAGCAGACGGCCTAACAGTCATGATA 502
QY 440 ATCACAAATGGAAACATGACCATATTAGGCATTATAATGGAGGGATTAAATAGAA 381
Db 503 ATCAACACTGGTGTATGACGACGAGCCGACTTATGGCAATGAAACATCTGGC 562
QY 380 ATATACAGGAAATATCAATAAAAACCCATATGAAACAGCTGGTCCATAATAAGA 321
Db 563 AATATCAGGAAATATCAATAAAAACCCATATGAAACAGCTGGC 609
QY 320 CATCACAAATGAAATTAACACAAATTAATGCAATAGTCATGATGGC 274

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RESULT	9	CB2859348/C	773 bp	DNA	linear	GSS	27-JUL-2005
LOCUS	CB2859348	OC_Ba0251M04.f OC	Ba	Oryza	coarctata	genomic	Clone OC_Ba0251M04
DEFINITION	5'	' genomic survey sequence.'					
ACCESSION	C2859348						
VERSION	C2859348.1	GI:71334104					
KEYWORDS	GSS.						
SOURCE	Oryza coarctata (Porteresia coarctata)						
ORGANISM	Eukarya; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;						
REFERENCE	Enhalioideae; Oryzeae; Oryza.						
AUTHORS	1. (bases 1 to 773)						
JOURNAL	Kim, H., Collura, K., Wissottoki, M., Byrne, M., Stum, D., Smart, D., Rao, K., Luo, M., Jetty, R., Kudrna, D., Muller, C., Soderlund, C. and Wing, R.						
COMMENT	OMAP (Oryza Map Alignment Project) - Arizona Genomics Institute Unpublished (2005) Contact: Rod A. Wing						
FORWARD:	TAA TAC GAC TCA CTA TAG GG						
BACKWARD:	CAC TCA TTA GGC ACC CCA						
PLATE:	0251	row: M	column: 04				
SEQ PRIMER:	TAA TAC GAC TCA CTA TAG GG						
CLASS:	BAC ends.						
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Db	/clone=OC_Ba0251M04"						
QY	/tissue_type="leaves"						
QY	/dev_stage="mature"						
QY	/lab_host="DHL0B"						
Db	/clone_lib="OC_Ba"						
Db	/note="Vector: pAGBAC1; Site_1: HindIII; Site_2: HindIII"						
ORIGIN							
	Query Match	4.0%	Score 39.6;	DB 10;	Length 773;		
	Best Local Similarity	48.3%	Pred. No. 4.5;	Mismatches 0;	Indels 0;	Gaps 0;	
	Matchees	111;	Conservative				
	716	TAGAGCCGGGGCCATGAAACGAAAGGTGTTAACGCCGCTTTCATTGCGAATA	775				
	230	TAACACGATTCGCTTGACTGGACCATATCACCGGGAGTGAGTGTGAAACCAAC	171				
	776	TGACGATACAAAGCGCGTGTGACAGAGAGAGACGAATTATTAACGCAATA	835				
	170	TACGCAACACAGATCAGATAATACAGGTTAAAGTGTGACTACTTTATCTGAAATT	111				
	836	CTTCGGTGTGACAGAACACTGGAACTACTATTCACCACTATGACATCGCAA	895				
	110	GCATCATTTGCTCTGCAAAATATAATTATTATGCAATTAGACGATCGCAA	51				
	896	TCCAAAAGTAATTATTCTGAGACCTTGACTGTGAGGCTAA	945				
	50	TGAAAGATAAAACATGCTCTATAGAGGTTCTGCGCAAAGATAA	1				
RESULT	10	CC254220/c	1055 bp	DNA	linear	GSS	13-MAY-2003
LOCUS	CC254220	CH261-4N24_Sp6.1	CH261 Gallus gallus	genomic clone	CH261-4N24,		
DEFINITION		genomic survey sequence.					

COMMENT	Determination of this BAC-end sequence was carried out as part of a collaboration with the Berkeley Drosophila Genome Project (BDGP). The BDGP is constructing a physical map of the <i>Drosophila</i> melanogaster genome using these BACs. For further information please see http://www.fruitfly.org . The BDGP Drosophila melanogaster BAC library was prepared by Kazutoyo Ooegawa and Aaron Mammone in Piero de Jong's laboratory in the Department of Cancer Genetics at the Roswell Park Cancer Institute in Buffalo, NY. The library is named RPCL-9B and was constructed by partial EcoRI digestion of <i>Drosophila</i> DNA provided by the BDGP from the isogenic strain Y2, cn bw sp, the same strain used for the BDGP's P1 and EST libraries. A more detailed description of the library, and how to order individual BAC clones, the entire library, or filters for hybridization from the BACPAC Resource Center can be found at http://bacpac.med.buffalo.edu/drosophila_bac.htm .
FEATURES source	<p>ORIGIN</p> <p>Query Match 3.9%; Score 38.6; DB 10; Length 1101; Best Local Similarity 15.6%; Pred. No. 9.9; Matches 47; Conservative 127; Mismatches 128; Indels 0; Gaps 0;</p> <p>Db 118 TGGACAGTCAGCTGACCGAGGGCCATAGAACAGTACGCCGTTTACGGATGG 177 /mol_type="genomic DNA" /db_xref="taxon:7227" /clone="BACR1F03" /clone_lib="RPCI-9B" /note="end : T7"</p> <p>ORIGIN</p> <p>Query Match 3.8%; Score 38.2; DB 11; Length 575; Best Local Similarity 50.3%; Pred. No. 11; Matches 94; Conservative 0; Mismatches 93; Indels 0; Gaps 0;</p> <p>Db 796 GTGATAACGGAGGACCAATTCAATACCCATTAACTCCGTATGTCAGCAA 855 /mol_type="genomic DNA" /db_xref="taxon:10090" /clone="MHP61J02" /clone_lib="MHP"</p>
FEATURES source	<p>ORIGIN</p> <p>Query Match 3.8%; Score 38.2; DB 11; Length 575; Best Local Similarity 50.3%; Pred. No. 11; Matches 94; Conservative 0; Mismatches 93; Indels 0; Gaps 0;</p> <p>Db 466 GAGCACATGGAGAACATAATCAGCACACAAACACAGACAGAATGTCAT 347 /mol_type="genomic DNA" /db_xref="taxon:10090" /clone="MHP61J02" /clone_lib="MHP"</p> <p>RESULT 14</p> <p>LOCUS BQ266623</p> <p>DEFINITION NISC_ff14b04.x1 NCI_CGAP_Mam5 Mus musculus cDNA clone IMAGE:2865727</p> <p>ACCESSION BQ266623</p> <p>VERSION BQ266623.1 GI:20491688</p> <p>KEYWORDS EST</p> <p>SOURCE Mus musculus (house mouse)</p> <p>ORGANISM Mus musculus</p> <p>REFERENCE Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Muridae; Murinae; Mus.</p> <p>AUTHORS Sciuognathi; Muridae; Muridae; Murinae; Mus.</p> <p>TITLE NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.</p> <p>JOURNAL National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997)</p> <p>COMMENT Contact: Robert Strausberg, Ph.D. Email: crapsb-r@mail.nih.gov Tissue Procurement: Lothar Heinrichausen/Robin Humphreys cDNA Library Preparation: Life Technologies cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LINN DNA Sequencing by: National Institutes of Health Intramural Sequencing Center (NISC) Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LINN at: infoimage.lnnl.gov Plate: LIAm7070 row: C column: 8 Seq primer: -21M13 forward primer (ABI). Location/Qualifiers</p> <p>1. . 593</p> <p>FEATURES source</p> <p>/organism="Mus musculus" /mol_type="mRNA" /strain="mix FVB/N, C57BL/6J" /db_xref="taxon:10090" /clone="IMAGE:2865727" /tissue_type="tumor, gross tissue" /dev_stage="7 months" /lab_host="DHIOB" /clone_lib="NCI_CGAP_Mam5"</p>
REFERENCE	Mammalia; Eutheria; Burchontoglires; Glires; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 575)
AUTHORS	Adams, D.J., Blige, P.J., Cox, A.V., Davies, R.M., van der Weyden, L., Jonkers, J., Smith, J., Plumb, R.W., Taylor, R.G., Nishijima, I., Yu, Y., Rogers, J. and Bradley, A.
TITLE	Direct Submission
JOURNAL	Submitted (20-FEB-2004) Sanger Centre, Hinxton, Cambridgeshire,
RESULT 13	<p>LOCUS CR008507/c</p> <p>DEFINITION 575 bp DNA linear GSS 05-JUL-2004</p> <p>FORWARD strand read from insert in 3'HPRT insertion targeting and chromosome engineering clone MHP61J02, genomic survey sequence.</p> <p>ACCESSION CR008507</p> <p>VERSION CR008507.1 GI:49741498</p> <p>KEYWORDS GSS; genome survey sequence; MICER.</p> <p>SOURCE Mus musculus (house mouse)</p> <p>ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;</p>

note="Organ: mammary; vector: pCMV-SPORTS; Site_1: SALL; Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"

H.O. and Venter, J.C. (Making small insert libraries for whole genome shotgun sequencing projects. In *Genome Sequencing: A Practical Approach*, eds. M. Vaudin and B. Barrell, Oxford University Press, 1999).

Query Match	Score	DB	Length
Best Local Similarity	49.3%	3	593
Matches	100;	Conervative	0;
		Mismatches	103;
		Indels	0;
		Gaps	0
Y	7.21	CCGGGGCGGATGAAACGAAAGGTGTACAGCGCTTCAATTGGCAATATGACG	780
b	192	CCCCCCCCAAAAAAAACCCCTTTCATAAAAAAAACCTT	251
y	7.81	ATACCAAGGCCAGTGATAACGGAGAGACGAATCATATAGCAAATACTCC	840
b	252	TTAACAGGCAAAAMAAATTGGGSGGAAAGGGGGGAAACTTG	311
y	8.41	GTGATGTGCACGAAACTGGAAACTACTATATTCCACCACTATGACAATGCCAATC	900
b	312	GAAGAAGGAAAGAAAGTTAAATTTTAAAGAAAGGCTTTAA	371
b	9.01	AAAGTAATTATTCTGTGAGA	923
y	372	AAAAAAATTTTTAAAGAA	394

Search completed: March 18, 2006, 13:11:49
Job time : 4770 secs

LOCUS AZ669903 DNA linear GSS 14-DEC-2000
DEFINITION ENTAMOEBA histolytica Sheared DNA Entamoeba histolytica
ACCESSION genomic genomic survey sequence.
VERSION AZ669903
GSS AZ669903.1 GI:11807049
KEYWORDS
SOURCE Entamoeba histolytica
ORGANISM Entamoeba histolytica
ENTAMOEBA
BUKARYOTA
ENTAMOEBIDAE
ENTAMOEBA
REFERENCE 1 (bases 1 to 853)
AUTHORS Loftus,B., Van Aken,S. and Fraser,C.
TITLE Determination of clone end sequences from Entamoeba histolytica HMI:IMSS sheared DNA library
JOURNAL Unpublished (2000)
COMMENT Contact : Brendan J Loftus
 Department of Eukaryotic Genomics
 The Institute for Genomic Research
 9712 Medical Center Dr., Rockville, MD 20850, USA
 Tel: 301 835 0208
 Fax: 301 838 3543
 Email: bjl0ftus@tigr.org
Clones are derived from the Entamoeba histolytica HMI:IMSS sheared DNA library
Seq primer: M13-Forward
Class: shotgun
High quality sequence start: 66
High quality sequence stop: 746.
FEATURES
Source
I. 853
Location/Qualifier
/organism="Entamoeba histolytica"
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/clone_lib="Entamoeba histolytica Sheared DNA"
/note="Vector: pHO51; Site 1: Bst I; Constructed at The
Institute for Genomic Research (TIGR), Rockville, MD.
Genomic DNA isolated from broth cultures of E. histolytica
using a method described by Clark and Diamond (Clark,
C.G., and Diamond, L.S. (1993) Entamoeba histolytica: a
method for isolate identification. Exp. Parasitol.
77:450.) The DNA was mechanically sheared to give a
tight size distribution (~2 kbp). The v + i method used for
the library construction is described in detail in Smith,

Qy 302 TCCCCGATGACTTGTGACATGGGTCCTGTCACTCTGGAAAGACGTAAG 361
Db 305 CACCTTGAGGAGTTATGTGTTGGGTTAGGTTAATAAGATTAGGAATTAAAC 364
Qy 362 AAAGAGTTAACAAATCAATTTATGAAAGAAATAACCACTTGATCATCGTTAC 421
Db 365 AAAGAGTTAACAAATCAATTTATGAAAGAAATAACCACTTGATCATCGTTAC 424
Qy 422 CGCTTCACTGATATGTCAGACCGACGGCCGAAACCTGGAGTAGACCAAGAG 481
Db 425 CTTTCATTCATGGTCACTTGATGAAACAGACATCCGTGACCTCACAATG 484
Qy 482 AGGGCTCAAGTCATGATACACCTGGTGTGACGCCACAGCCCGACTTAT 541
Db 485 GCTTAATTAAGTTAAAGATAATTATGTTTACCTAACAAATGACCTTAAT 544
Qy 542 GGCATOTAAACAACTGCAAGGATAACAGGATACAGGATCACGCCAGAAC 601
Db 545 AGATGGGCGGATTAACCTTCTGCTTTSGCCAAGGCTTGGAACTGTGTCGG 661
Qy 602 AGATGGGCGGATTAACCTTCTGCTTTSGCCAAGGCTTGGAACTGTGTCGG 664
Db 605 TAATGGTAAAGTGCTAGTAAGATCATGCGCTGTGAAAGGAACTACCAAT 604
Qy 662 GGGATTTACCCGCTTCCGGTTGTCAGGCTTATGAAAGAACATCTAGAGC 721
Db 665 GTGGTTATACGTCACAGATGTTTACCGCTACATTTAACACCAACTACGT 724
Qy 722 GGGCGCCGATGAAACGAAGGGTGTACAGCGCTTCAATTGGCAATATGAC 781
Db 725 GTTCCCATATGAGTGAATTATGAAATGTTAGATGTTAGATCTAGCTAGA 784
Qy 782 TACCAAGGGCGCAGTAAAGGAAAGGGAATTCAATGCAATTATTCGG 841
Db 785 TCCCTCAAGGGCAGTAT--CGATGCCATTAACTACACACATATCATTAG 841
Qy 842 TGATGTCAGGAAACTGGAIACTTACCACTATGACAACTCGCAAATCCAA 901
Db 842 TGATGTCAGGAAACTGGAIACTTACCACTATGACAACTCGCAAATCCAA 901
Qy 902 AAGTAATTTCATGAGA 920
Db 902 AAATAAAATTAACTGAGA 920

RESULT 2

US-09-134-001C-2421

; Sequence 2421, Application US/09134001C
; Patent No. 6380370

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: GTIC-007

CURRENT APPLICATION NUMBER: US/09/134,001C

CURRENT FILING DATE: 1998-08-13

PRIOR APPLICATION NUMBER: US 60/064, 964

PRIOR FILING DATE: 1997-11-08

PRIOR APPLICATION NUMBER: US 60/055, 779

PRIOR FILING DATE: 1997-08-14

NUMBER OF SEQ ID NOS: 5674

SEQ ID NO 2421

LENGTH: 996

TYPE: DNA

ORGANISM: Staphylococcus epidermidis

US-09-134-001C-2421

Query Match 16.0%; Score 159; DB 3; Length 996;
Best Local Similarity 49.8%; Pred. No. 1.4e-39;
Matches 458; Conservative 0; Mismatches 6; Indels 2; Gaps 2;

Qy 2 ATATGTCAGGAACTGCTACATGGAACTGTGACCTGACATGAAATTCAGA 61

Db 14 ATATGTCAGGCAATTCTATACAAACACGTTACCATATTAGCTGAGACAA 73
Qy 62 TGGATTTGCAATTTCAGGTGGGACAGGGTGTCTTATCGGGCGTTACAGCT 121
Db 74 TGGACTTCATTTGAAATTAATGTTTACCGTACGCTTCAAGCGCAATTACTAC 133
Qy 122 ACAGTGAAGCTACGGAGGGCCATCGACAGACAGTGGGTATCGTATGGGAGA 181
Db 134 AATTGATCTAGATTCAGACATGCTTCAATTGTTTACCGTACGCTTCAAG 190
Qy 182 AACCTGGAAATATATATGCGACGGCATTATGAAAGCGTTATCTGCGGGCG 241
Db 191 AAGTAGGAGGTATAGATTTGGTGTGTTACGAAAGCTTACCTTCAGACC 250
Qy 242 TTATTTTCCGGGTTATGGGAGTACAGGAAACGATGGGAGATACCGTTACATG 301
Db 251 ATTACTCTGTGAAAGCTCATACAGTACCTACACGTTAGTTTACTTG 310
Qy 302 TCCCGCATGAGTTGTCATGAGGTGCTGAGCTTGTGAGAGCTTACATTGAC 361
Db 311 CACCTGGAGGTTTATTGTTGGTTTAAATTAAGGTTAGTACGGAAATTAAAC 370
Qy 362 AAAGATGTCATTTAACGATGTTAGGAAATTTAGATCATGTTACAGTTAC 421
Db 371 AAAGGTTAGAAATCAATTATGATGAAAAAATACGACTTGTGATATGTTCTC 430
Qy 422 CGCTTCATCGGATATGTCAGACGGAGGGCCGAAACTGAGGATAGACAGAG 481
Db 431 CTTCATTCATGTCATGTTACGTTACGCAATACGTTACGGCATAGCTCACATG 490
Qy 482 ACGGCTCAAGTCATATAATCAACCTGGCTCATCGAAGCGCTTAACTGAG 541
Db 491 GCTTATTAATGTTAGAATAATTGTTACATCTTAACTTAATGAACTTAATTGATT 550
Qy 542 GGATGTCACCATCTGGCAATATACAGGAATCAGCCGAGGAACTGGCTACCG 601
Db 551 GGCATCTCTACTTACGTTACGCTTGTGTCATCGAAGCGCTTATAT 610
Qy 602 AGATGGCGGATAGCCCTCTGCTTGGCAAGGTTAGGACTGTGGTGTGCGG 661
Db 611 TAATGGTAAAGTGCTAGTGTAGATCAACGGCTGTGAAAGCAGGAACTGGCTACCG 670
Qy 662 GGGATTTACCCSCTTCCGGTTGTGAGGAGCTTACGGCTTACATATTAGAC 721
Db 671 GTGGTTATAGTCACAGATCGTTATAGCGCTTACATATTAGACCAACTACGT 730
Qy 722 CGGGCCGATGAAAGGAGGCTAACAGCCGTTCAATTGCGAAATATGACGA 781
Db 731 GTTCCCATATGAGTGAATTATGAAATTGTTAAGTTCTGAAATCTAGCTAGA 790
Qy 782 TACCAAGGGCGCAGTAAAGGAAAGGGAATTCAATGCAATTACGCAATAC 841
Db 791 TCCCTCAAGGGCAGTAT--CGATGCCATTAACTACACATATCAATG 847
Qy 842 TGATGTCAGGAAACTGGAIACTTACCACTATGACAACTCGCAAATCCAA 901
Db 848 TGATGTCAGGAAACTGGAIACTTACCACTATGACAACTCGCAAATCCAA 907
Qy 902 AAGTAATTTCATGAGA 920
Db 908 AAATAAAATTAACTGAGA 926

RESULT 3

US-09-710-279-3345/C

; Sequence 3345, Application US/0910279
; Patent No. 6703422

GENERAL INFORMATION:

APPLICANT: KIMMELLY, WILLIAM JOHN

TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLBIC ACIDS AND PROTEINS

FILE REFERENCE: P334800

CURRENT APPLICATION NUMBER: US/09/710,279

CURRENT FILING DATE: 2000-11-09

PRIOR APPLICATION NUMBER: 60/164,258
 PRIORITY FILING DATE: 1999-11-09
 NUMBER OF SEQ ID NOS: 4472
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 3345
 LENGTH: 2975
 TYPE: DNA
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-710-279-3345
 Query Match Similarity 16.0%; Score 159; DB 3; Length 2975;
 Best Local Similarity 49.8%; Pred. No. 2.5e-39; Mismatches 455; Indels 6; Gaps 2;
 Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
 Qy 2 ATATGGCACCAAGCTTACAGCTGGAAACTGCTGGTAACTGTAGTTAGCAGAACAA 61
 Db 1755 ATATGGTGTACTGCCATTCTTATACTACAAACAGTTCACATTATGCTAGAACAA 1696
 Qy 62 TGCATTTGCAATTTCAGCTGGGACAGAGGTGATCTCTATCGGCGGTACAGCTGA 121
 Db 1695 TGGACTTGTGAACTTGAATTGATCCAAACATTGTCAGGCGATTATCTGCGGCC 1636
 Qy 122 ACAGTGANGCTGAGGGAGGCCATCAGAACACAGTACCGTTATCGGTATGGAGAA 181
 Db 1635 AATTTGATCTAGATTCAGAACATGCTT---GRATATGTTTGTGAGAACATTAA 1579
 Qy 182 AACCTGGAAATAATTGTCGACGGGATTATGAAAGCGGTATCTGCGGCC 241
 Db 1578 AACTTAGGAACTTATAGATTGGTGTGTTAAGAACAGTTAGCTATTGCAACC 1519
 Qy 242 TTATTTCCGGGACTATCGGAGCTAACGTTACCTAACATAGCTTACATG 301
 Db 1518 ATTACTTACCTGGTGTGACATGGCTGCTACTCTGTCAGCTTGGAAAGCTAAAG 1459
 Qy 302 TCCGGCATGAGTTGTGACATGGCTGCTACTCTGTCAGCTTGGAAAGCTAAAG 361
 Db 1458 CACCTGAGGAGGTTATTGTTGGTTTAATTAAGTATAGCTAGCGGAAATTAAAC 1399
 Qy 362 AAAGAGATCGACCTTAACTGAGTGTAGAGAAATTAGCTATGATCACAGTTAAC 421
 Db 1398 AAAGAGTGTAGAACATCATATATGATGAAAGAAATTAGACTTGTATGTTCTC 1339
 Qy 422 CCGTCACTGGTATTGCAAGCCGGAGGGCGGAACCTGGATAGAACAGAGCAG 481
 Db 1338 CTTACATTCATGGTCACTGATGAAACAGGACATACGGTACGAACTTCACATG 1279
 Qy 482 ACGGCTCAAGCTATGATAATCACCTGGTGTCTAGAACAGCCGGACTTAT 541
 Db 1278 GCCTTATTTAGTAAAGATAATTATGTGTCACTTAAACATGACCTAATTAGATT 1219
 Qy 542 GGATGACACAACTGAGCAATAAGAACAGTACAGGAACTGTTGGCGCG 601
 Db 1218 GGCACTATCTAACTTAAAGAACATTAACCTTAAACAAAGCTTAAACATCAAT 1159
 Qy 602 AGATGGCGGATTAGCCCTTCTGGTTGGCAAGGGTTAGGAACTGTTGGCGCG 661
 Db 1158 TATAGGTTAAAGTGTAGTAGATACTAAGTGGTGTGAGGAAACAACTTACGG 1099
 Qy 662 GGGATATACAGCCTTCGGTTGGTGTGTTATGAAAGAACATCTAGAGC 721
 Db 1098 GGTTTATAGCTAACAGATCGTTTATACGGCTCACTTAAAGAACACTACGCT 1039
 Qy 722 CGCGGGCGGATAACCAAGGTTACAGGAGCCCTTCAATTGGCAATATGAGGA 781
 Db 1038 GTTCCCTTAATGAGATGAAATTAACTGTTAAGTTGTTAGAATCTAGTCAGTA 979
 Qy 782 TACCAAAAGGGCGAGTGTAGTACCGAGAGGAAATTCATATACCAATACTTCG 841
 Db 978 TCCCTCAGGTCAGTGT---CGATCCATTAACTACATACACAGATCAATTAG 922
 Qy 842 TGATGTGCAAGAACACTACTTCCACCATATGACAATGGCAATCCCAA 901
 Db 921 TGTGGAGAGTAAAGAGAAGGTTATTAAGCCCTACTTTAGCAATCAATTCA 862
 Qy 902 AAGTAATTATTCATGA 920
 Db 861 AAATTAATTAACTGAGA 843
 RESULT 4
 Sequence 4184 Application US/09710279
 ; Sequence 4184 Application US/09710279
 ; Patent No. 6703492
 ; GENERAL INFORMATION:
 ; APPLICANT: KIMMELER, WILLIAM JOHN
 ; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
 ; FILE REFERENCE: P3480US
 ; CURRENT APPLICATION NUMBER: US/09/710,279
 ; CURRENT FILING DATE: 2000-11-09
 ; PRIOR APPLICATION NUMBER: 60/164,258
 ; PRIOR FILING DATE: 1999-11-09
 ; NUMBER OF SEQ ID NOS: 4472
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO: 4184
 ; LENGTH: 4114
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: synthetic
 US-09-710-279-4184
 Query Match Similarity 16.0%; Score 159; DB 3; Length 4114;
 Best Local Similarity 49.8%; Pred. No. 2.9e-39; Mismatches 455; Indels 6; Gaps 2;
 Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;
 Qy 2 ATATGGCACCAAGCTTACAGCTGGAAACTGCTGGTAACTGTAGTTAGCAGAACAA 61
 Db 1626 ATATGGTGTACTGCCATTCTTATACTACAAACACTTACATTATTAGCTAGAACAA 1685
 Qy 62 TGCATTTGCAATTTCAGCTGGGACAGAGGTGATCTCTATCGGCGGTACAGCTGA 121
 Db 1686 TGGACTTGTGATTGACATGGTACGACATGGCTT---GAATATGTTGTGAGAACATTAA 1745
 Qy 122 ACAGTGANGCTGAGGGAGGCCATCAGAACAGTACCGTTATCGGTATCTAC 181
 Db 1746 AATTTGATCTAGTTGACATGGCTT---GAATATGTTGTGAGAACATTAA 1802
 Qy 182 AACCTGGAAATAATTGTCGACGGGATTATGAAAGGGTTATCTGCGGCC 241
 Db 1803 AAGTAGGAGCTTATGATTTGGTGTGTTAAACAAAGGTGTTAGCTATTTCGAC 1862
 Qy 242 TTATTTCCGGCTTGGGAGTACGGAAACGATACGGGAAGATACCGTTACATG 301
 Db 1863 ATTACTTACUGTGTGAGCTACGGTGTGTTAGGTTACCTAAAGTATTTACTTAG 1922
 Qy 302 TCCGGCTTGGGAGTACGGTGTGAGCTACGGTGTGTTAGGTTACCTAAAGTATTTACTTAG 361
 Qy 1923 CACCTGGGGAGTTATGTTGGTTAGGTTACCTAAAGTATTTACTTAGGTTACATG 1982
 Db 362 AAAGATGTCGATCTTACGATGTGAGGAAAATTAGATCTATGATACAGTTAC 421
 Db 1983 AAAGGTTAAGAAATCTAAATTATGATGAAAAATAACGACTTGTATGTTCTC 2042
 Qy 422 CGCTGACTGGTACGTTGAGCCGGAGGGCGGAACCTGAGATGACCAAGGAG 481
 Db 2043 CTTACGTTCTGATGGTCACTGATGAAACAGACATACGGTACGCTATGAACTCACATG 2102
 Qy 482 ACGGCTCAAGCTATGATACAGCACTCTGGTGTAGACAGCCCCGACTTAT 541
 Db 2103 GTTATTATGTTAAAGAAATTGTCACCTTAACTTAACTAACATGAACTTAATTGATT 2162
 Qy 542 GGCATGTAACCAATCTGCGCAATAACAGAACTGAGCCGAATTAGAGAGCAAG 601

SEQUENCE DESCRIPTION: SEQ ID NO: 444;

TOPOLogy: linear

STRANDEDNESS: double

US-08-956-171E-444

Query Match 14.7%; Score 146; DB 3; Length 11466;

Best Local Similarity 47.5%; Pred. No. 6.3e-35; Mismatch 0; Indels 3; Gaps 1;

Matches 468; Conservative 4; Score 146; DB 3; Length 11466;

Qy 602 AGATGGCGGATTAGCCCTTGTCTTTGCCAAGCTTAGGAATGTTGGCTCGCGG 661

Db 2223 TAATAGTAAGTGTCAAGTCAATGGCTTAAGGAAATCAACCAATCAAT 2222

Qy 662 GGGATATACACCGCTTCCCGTTTCAGCTGTTTGTAGCATATGGCTCGGG 721

Db 2283 GTGGTATACGTCACAGATCGTTACGGCTATTTAGAACAGACTCTGGC 721

Qy 722 CGGCSCCGATGAAAGAAAGCTGTAACGGCTTCAATTGGCAATATCGA 781

Db 2343 GTTCCATATGAGAAGAAATTAAATGAAATGTTAAAGAACACCAACTAGCT 2342

Qy 782 TACCAAGGCGAGTGAACGGAGAGCAATTATGAAATTCGAAATATCGA 841

Db 2403 TCCTCAAGGTCAGTAT--CGATCCATAATACATACACAAATCAATTAG 2459

Qy 842 TGATGCGAACCAAATCTGGAAACTATATTCCACCACTATACACAATCGA 901

Db 2460 TGTGCGAAGTAAAGAAAGAGTATATATAGCTTACCTAGCAATCGAATTCA 2519

Qy 902 AAGTAAATTATTCGTA 920

Db 2520 AAATAAAATTAATCTGAGA 2538

RESULT 5

US-08-956-171E-444/C

; Sequence 444, Application US/08956171E

PATENT NO. 6593114

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Farnon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPUTER: HP Vectra 486/33

OPERATING SYSTEM: MSDOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/956,171E

FILING DATE: 20-Oct-1997

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1995

APPLICATION NUMBER: 08/781,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

REFERENCE/DOCKET NUMBER: PB248P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 11466 base pairs

TYPE: nucleic acid

Qy 3451 TATTCCGGAGGTATAGTCATATGGTCACACAAAGGGAGATACGGTACATTC 303

Db 304 CGCGCATGAGTTGTGACATGCGTCAGCTGTCTTGAGACGTTAAAGAA 363

Db 3391 CAATATGAAATTGTGACATGGTTGGATATACACAGGATGAGATGAA 3332

Qy 364 AAGATTCGATCTTAACGATTTAGATGAAATAGCTCTTGTGATCACATTACG 423

Db 3331 CAGCAATCCAAATACATGTTGTTAGCTTAAATGACATGGTAAAGTCCGCA 3272

Qy 424 CTTCACCTGGATTTGTGAGACGGACGGCCAACTGACCATAGACCGAC 483

Db 3271 TGCATTTACGTTTCGATGAACTGGACATACCTGGATTTGGATATGAGGT 3312

Qy 484 GCCTCTAAGTGTATGAAATACATGTTGTTAGCTTAAATGACATGGTAAAGT 543

Db 544 CTGTAAACACTGGCAAAATACAGGAACTGGCTGATGAGAACAGCCGACTTTATCG 603

Db 3211 GAGGTGGTTAAAGATAATCTATTGGTGTAAACAAATCCGAGCTTAAATG 3152

Qy 3151 CATTATGTTAAAGACATATATCATATTCCTTATACGACACGAAATTAA 3092

Db .604 ATGGCGGATACCCCTCTCTGGCAAGCTGGCTTGGAGCTTGGTCTCCGGG 663

Db 3091 TTGGAAAGGTGAACTGGATGAACTTGGCAATGAGCGGGTACATTGGTGGCAAGT 3032

Qy 664 GATTTACACCCCTTCGGGTTGTGAGGCTGTTATGGAAAGAACATCTGAGCG 723

Db 3031 GAGTTACTTCGACTGGCTTGTGAAATGACATTTGGAAAGCAACTCTGCA 2972

Qy 724 GCGGCCGATGAAACGAAAGGTGAACTGGCTGAGCGCTTCAATTGGCAATATGACGATA 783

Db 2971 AACATGATAAAAGAAATGATTATGATGATGATGATGATGATGATGAAATAATA 2912

Qy 784 CCGAAAGGGGAGTGAACGGAAAGCAATTGGCAATGAGCAATATCTGGC 843

Db 2911 CGATGGGATGTTACGTCGCGATGATCTGAGCAATCTGAGCTTACGACGATA 2852

Qy 844 ATGGCGAAGGAACTGGAAACTTACATTCACCACTATGACATGCGCAATCCAAA 903

Db 2851 ATAAATTAACTACGAGGAGCTTACATTTAGCTTATGAGCTTGGCAATATGAGA 2732

Qy 904 GTAAATTATTCGAGGACCTGACTGTTGAGCTTAAGTGTGTTCCGTAAGA 963

Db 2791 TAAAGTCACAGTGTAAATAGAAAGATATGACGATTTAACGCCCTGAGAG 2732

RESULT 6 US-08-781-986A-444C
 Sequence 444, Application US/08781986A
 Patent No. 6737248

GENERAL INFORMATION:

APPLICANT: Charles Kunsch
 TITLE OF INVENTION: *Staphylococcus aureus* Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
 ADDRESSEE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville
 STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MS-DOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781, 986A
 FILING DATE: CLASSIFICATION: 435
 PRIORITY APPLICATION DATA:
 REGISTRATION NUMBER: 30, 446
 REFERENCE DOCKET NUMBER: PB248PP

TELECOMMUNICATION INFORMATION:
 TELEFAX: (301) 309-8804
 INFORMATION FOR SEQ ID NO: 444:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 11466 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 US-08-781-986A-444

Query Match 14.7%; Score 146; DB 3; Length 11466;
 Best Local Similarity 47.5%; Pred. No. 6, 3e-35;
 Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

Qy 4 ATGTGCAAGTCCTACATGGAAACCTGCTGACCGTAAACATGTTAGCATAGAACATG 63
 Db 3688 ATGTGACAGGTTCAACTTAATAAATCAAGRACTCTTGAGCCAGATG 3629
 Qy 64 GATTTGCATTCACTGGGACAGAGGTGAACTTGTACGGGCTTACGGTGAAC 123
 Db 3628 GATTATGATTCCATTAGATGGTTCGCCAGCTAACGCTTAAGAATTATGTTGAA 3569
 Qy 124 AGTGAGCTGAGGAAGGCCATCAGACAGCTAGCGTTATCGCTATGGGGAAA 183
 Db 3568 TCTTGTACT--GGCAGACAGGCCAACGRATATGGCTTATGGCACGGAGAT 3512
 Qy 184 CTGGAAATATATTATGCCGACGGATTATGAAAGCGGTTATCTTGTGGGGCTT 243
 Db 3511 ATGGAGTTTATTATGGCTGCTTATGAAATGCGCTTCAAGACAA 3452

Query Match 9.6%; Score 95,4; DB 3; Length 987;
 Best Local Similarity 45.8%; Pred. No. 1,6e-19;
 Matches 407; Conservative 0; Mismatches 476; Indels 6; Gaps 2;

Qy 964 GAGAGAGTATTGATGA 2706

RESULT 7 US-09-134-000C-838
 Sequence 838, Application US/09134000C
 Patent No. 6617156

GENERAL INFORMATION:

APPLICANT: Lynn Doucette-Stamm et al
 TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO FILE REFERENCE: 032796-032
 CURRENT APPLICATION NUMBER: US/09/134, 000C
 CURRENT FILING DATE: 1998-08-13
 PRIOR APPLICATION NUMBER: US 60/055,778
 PRIOR FILING DATE: 1997-08-15
 NUMBER OF SEQ ID NOS: 6812
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO 838
 LENGTH: 987
 TYPE: DNA
 ORGANISM: *Enterococcus faecalis*
 US-09-134-000C-838

Query Match 9.6%; Score 95,4; DB 3; Length 987;
 Best Local Similarity 45.8%; Pred. No. 1,6e-19;
 Matches 407; Conservative 0; Mismatches 476; Indels 6; Gaps 2;

Qy 41 AACGATATTAGCAGAACATGGATTTCAGCTGGGACAGGGTGAATCTT 100

Db 3391 CAAATGAAATTGATGGATACAAACAGGATGAACTTACAGGATGAACTA 3322
 Qy 364 AGATTCGATCTAACGATTTAGAGAAATTAGATCTATGGATACATGTTACG 423
 Db 3331 CAAAGCATCCAAATACATGTTGATGCTGATTAATGAAATCGGTGAAGTTCGCCA 3272
 Qy 484 CTTCACTGATATGTCAGACGGACGGCCAAACCTGACCATAGACCAAGCAGC 483
 Db 3271 TTGCAATTGATGTTGCACTGACATGTTGAGGT 3212
 Qy 544 CTGTAAACATTCTGCAGAACATACAGGAATCAGACCGAACTTGGCTTACG 603
 Db 3151 CAACTATGAACTTAACTTAAAGACAAATATCATATTCCTTAACTCAGACAGCAAATTA 3092
 Qy 604 ATGGCGATATTGCCCCCTCTCTTGGCCAGGCTTAGGAACTGTTGGTGGCCGGG 663
 Db 3031 GATTTACTTCACTGAGCGCTTGTGAGAATGGCTTATGAAAGCAGTAAATGG 3152
 Qy 724 GCGCCGATGAAACGAAAGGTTAACAGCCGTTCAATTGGCAATATGACGATA 783
 Db 2971 AACATGATTAAGAATGGTTAATGAACTTGGCTTATGAAAGACATCTAGACCCG 723
 Qy 784 CCAAAAGGGCGCTGTGATAACGGAGAGAGCGAAATTCATTATACGCAATATCTCCGTG 843
 Db 2911 CGATTTGAAATGTTACCTCCGGATGTCGCAATACATTAACGTTGCTGCAA 2972
 Qy 844 ATGTGCAACGAAACTGAACTACTATTCACCACTATGAAATGGCAATATGGCTG 8052
 Db 2851 ATAAATTAACTACAGAACAGCTTATGTTATGATGTTATGAACTTACGATGTA 2792
 Qy 904 GAAATTATTTCATGAGACCTTGTACTGTTGGAGCTAAGTGTITCCCTAAAGCA 963
 Db 2791 TTAAGCTCAAGATGATTTAAATAGAAAGATGAGCTTAAAGCTGAGAAG 2732
 Qy 964 GAGAGAGTATTGATGA 2706

Db 2731 CAAATGAAATTGATGGATACAAACAGGATGAACTTACAGGATGAACTA 2706

STATE: Massachusetts
COUNTRY: USA
ZIP: 02354

COMPUTER READABLE FORM

MEDIUM TYPE: CD-ROM ISO9660

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107, 532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085, 598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Arinieillo, Pamela Deniske

REGISTRATION NUMBER: 40, 489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5907

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 366:

SEQUENCE CHARACTERISTICS:

LENGTH: 978 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: circular

MOLECULE TYPE: DNA (genomic)

HYPOTHETICAL: NO

ANTI-SENSE: NO

ORIGINAL SOURCE:

FEATURE:

NAME/KEY: misc_feature

LOCATION: (B) LOCATION 1... 978

SEQUENCE DESCRIPTION: SEQ ID NO: 366:

US-09-107-532A-366

Query Match

Best Local Similarity 8.3%; Score 82.6; DB 3; Length 978;

Matches 363; Conservative 0; Mismatches 424; Indels 6; Gaps 2;

QY 197 TATTGCCAGGGATTATGAAACGAGGTACCGCCCTTC 760

Db 191 TTATTACGACAAATGAAAGATTGAGTCTCTTGTGAGTT 250

QY 257 ATGGGAGTACGAAACGATCGGGAGATCCGTACATGTCGGCTT 316

Db 251 ATGCTGATTATGAA--ATAGAGGGAGACATGATCTCTTGTGAGTT 307

QY 317 TGACATGCTGCTGCTGAACTTCCACT 376

Db 308 TCCCTTGAGTTAGGACATGTCACAGTAGGAGACTAAATTTAAATA 367

QY 377 TAACATGTTAGGAAATTAGATCATGGTGTACGTTACCGCTACGGAAT 436

Db 368 TCAATTACAAATTATTAATAGTGTGAACTTCCATTACATGGCTAT 427

QY 437 TGTGAGCCGGACGGCGAACCTGACGATAGACCAAGAGCGACGCCCTCAAGCT 496

Db 428 TAGCTGAT--AAGAAATTCAATTGCTGATGAAAGATGATGACTCTATAT 484

QY 497 ATGATAATGACCTGCTGCATGAGAAAGACGCCGAACTTATGGCTGTAACATC 556

Db 485 ATGATAACCTGCTGCATGAACTTATCCCTCAATTGACTATCAATTAAATT 544

QY 557 TCCAGCAATACAGGATCAGCGGAAATTAGAGAGAGATGGCGGATG 616

Db 545 TAACATGCTGCTATGAGTGTAACTCTAAATAATTCAATCAAATA 604

617 CCCTTCGTTGGCCAGGTTAGGAACTCTAAATAATTCAATCAAATA 676

RESULT⁸

US-09-107-532A-366 Application US/09/107532A

; Sequence 366 Application US/09/107532A

; Patent No. 6583275

; GENERAL INFORMATION:

APPLICANT: Lynn A. Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEAR ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROCOCCUS FAECIUM FOR DIAGNOSTICS AND THERAPEUTICS

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESSEE: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Waltham

STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 3720:
US-08-956-171B-3720

Query Match 4.8%; Score 47.8; DB 3; Length 400;
Best Local Similarity 48.1%; Pred. No. 0.0001; Mismatches 147; Indels 0; Gaps 0;
Matches 136; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

Db 605 GTTGAATGCTATGCCGGTATGGAGGATAGCTTCCTGGAGATTATCCTAG 664 ;
Qy 677 CTTCCCGGTTGTCAAGAGCTTATTGAAAGAACATCTAGAGCGGGCGGAGA 736 ;

Db 665 TATCTGTTTGTAAAGCACTTACAGAGCTGATTGAGATTCAGGGAGATCAGT 724 ;
Qy 737 CGAACGGTGACAGCGCTTCAAATTGGCAATATGAGATACCAAGGGCGAG 796 ;

Db 725 CAGAAAGTATAAGTCATTTCCATATCTTAGTTAGGTCAAGAACACAAAAGTTG 784 ;
Qy 797 TGATTAAGGAGAGGAGAACTTACGAAATATAGCAATATTCCTGATGTGACAGAA 856 ;
Db 785 GTGAGTGTGATGAGAAATATGATAATCAATTATTCCTGTTGCAATGTGACA 844 ;
Qy 857 CTGGAACATCTATTCACACTATGACATACGATCAGCACTGCAAAAGGAAATTTC 916 ;
Db 845 AGGAACTTATATGAGACATATGAGACAGTCAAATACGCAATGATGAATA 904 ;
Qy 917 ATGAGACCTGACGTTGAGCTTAAGTGTTCGGCTAACAGAGAGAGTTC 976 ;
Db 905 AAGAGACTTATGATAGTCATAAGTTATGTTATCCAAATATAGAAACACAAATTA 964 ;
Qy 977 ATGAGCTTA 989 ;
Db 965 AATATATAATTA 977 ;

RESULT 9
US-08-956-171B-3720/C
Sequence 3720, Application US/08956171E
Patent No. 6593114

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
Gil H. Choi
Patrick S. Dillon
Craig A. Rosen
Steven C. Barash
Michael R. Fanon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5256

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

COMPUTER READABLE FORM:
ZIP: 20850

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
PRIORITY APPLICATION NUMBER: 60/009 861
APPLICATION NUMBER: US/08/956,171E
FILING DATE: 20-Oct-1997
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
NAME: Mark J. Hyman
REGISTRATION NUMBER: 46,789
REFERENCE/DOCKET NUMBER: PB248P1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (240) 314-1224
TELEFAX: (301) 309-8512
ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3720:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear

RESULT 10
US-08-781-986A-3720/C
Sequence 3720, Application US/08781986A
Patent No. 6737248

GENERAL INFORMATION:
APPLICANT: Charles Kunsch
TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
NUMBER OF SEQUENCES: 5255

CORRESPONDENCE ADDRESS:
ADDRESSEE: Human Genome Sciences, Inc.
STREET: 9410 Key West Avenue
CITY: Rockville
STATE: Maryland
COUNTRY: USA

COMPUTER READABLE FORM:
ZIP: 20850

MEDIUM TYPE: Diskette, 3.50 inch, 1.4MB storage
COMPUTER: HP Vectra 486/33
OPERATING SYSTEM: MSDOS version 6.2
SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/781,986A
FILING DATE:
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:

ATTORNEY/AGENT INFORMATION:
NAME: Benson, Bob
REGISTRATION NUMBER: 30,446
REFERENCE/DOCKET NUMBER: PB248PP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 309-8504
TELEFAX: (301) 309-8512
INFORMATION FOR SEQ ID NO: 3720:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
LENGTH: 400 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLGY: linear

Query Match 4.8%; Score 47.8; DB 3; Length 400;
US-08-781-986A-3720

Best Local Similarity 48.1%; Pred. No. 0.0001; Mismatches 147; Indels 0; Gaps 0; Matches 136; Conservative 0; Mismatches 147; Indels 0; Gaps 0;

Query Match 3.9%; Score 39; DB 2; Length 7218;
Best Local Similarity 5.8%; Pred. No. 0.28; Mismatches 24; Conservative 206; Mismatches 181; Indels 0; Gaps 0; Matches 24;

Db 286 GATACCGGTCACATGTCGCCGATGAGTTTGACATGGTGTGAGCTGCTCAGTCT 345
Db 333 GACCGGATGATAATTACGCAAATGAAATTGACATGGATTGGATATACACAGC 274
Db 345 TGCAGAGCTGAAGAAGAAGATTCGATCTTAAGATGAGAAATAGATCTA 405
Db 273 ATCGAGATGATGAAACACAGCAATCACAGCATTCCCAAATACATGTTGAGCTG 214
Db 406 TTGGATACAGTTAACCGCTTACTGGATATGTCAGACCGGCGGAAACCTGAGC 465
Db 213 ATCGTGAGNTTCGCCATTGCAATTATCATGTTGCGATGCAACTGGACATGCTGA 154
Db 466 ATAGAACCAAGAGCAGACGCGCTCAAAGCTATGATAATCACCTGGTCTATGACGAC 525
Db 153 GTTCATTAAGAGGGTAGGTATAAGATAACCTATTGGTCTAACATT 94
Db 526 AGCCCCGACTTATGGATGACCAACTGCGACAAATA 568
Db 93 CATCCGAGCTTAATTGGCATATAGTAATTAGAACAATA 51

RESULT 11
US-08-232-463-14/C
Sequence 14, Application US/08232463
; Patent No: 5670367
GENERAL INFORMATION:
APPLICANT: DORNER, F.
APPLICANT: SCHEIFINGER, F.
TITLE OF INVENTION: RECOMBINANT FOWLPOX VIRUS
NUMBER OF SEQUENCES: 52
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22311-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,463
FILING DATE: 2000-09-08
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/935,313
FILING DATE: 2000-09-08
APPLICATION NUMBER: US/07/935,313
FILING DATE: 2000-09-08
REFERENCE/DOCKET NUMBER: 29,768
NAME: BENT, Stephen A.
ATTORNEY/AGENT INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 836-9300
TELEFAX: (703) 683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 7218 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
CLONE: DTZPpe-F1s
US-08-232-463-14

RESULT 12
US-09-949-016-14834
Sequence 14834, Application US/09949016
; Patent No: 6812339
GENERAL INFORMATION:
APPLICANT: VENTER, J. Craig et al.
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
FILE REFERENCE: CLO01307
CURRENT APPLICATION NUMBER: US/09/949,016
PRIORITY FILING DATE: 2000-04-14
PRIORITY APPLICATION NUMBER: 60/1241,755
PRIORITY FILING DATE: 2000-10-20
PRIORITY APPLICATION NUMBER: 60/237,768
PRIORITY FILING DATE: 2000-10-03
PRIORITY APPLICATION NUMBER: 60/231,498
PRIORITY FILING DATE: 2000-09-08
NUMBER OF SEQ ID NOS: 207012
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 14834
LENGTH: 107140
TYPE: DNA
ORGANISM: Human
US-09-949-016-14834

Query Match 3.8%; Score 37,4; DB 3; Length 107140;
Best Local Similarity 49.7%; Pred. No. 3.7; Mismatches 95; Conservative 0; Mismatches 96; Indels 0; Gaps 0; Matches 95;

Query Match 3.8%; Score 39; DB 2; Length 7218;
Best Local Similarity 5.8%; Pred. No. 0.28; Mismatches 24; Conservative 206; Mismatches 181; Indels 0; Gaps 0; Matches 24;

Db 682 CGGTTGTCAGAGCTGTTTATGAAACATCTAGGCCGGCGCATGACAAA 741
Db 3534 CGTTTGAGGAGGAGTTTAAAMAAAAGGACAGAGGGCGATGTTAAAGAAAA 3593
Db 742 GGTGTAACAGCCGCTTCAATTGCAATATGCAATGACGATACAAAGGGCGAGTATA 801
Db 3594 AGGGAAACAGGAAATTGGTTCTGTAGAGGGTACCCAGAAAGACCTGTGGGTCTT 3653
Db 802 ACGGAGGAGACGAATATTATACGCAATATCTTGGTGTGATGTCAGAACTGGA 861
Db 3654 GCCATAGCAGTTACCTTGTAAACAGAAACATCCCATAACTCATGATTG 3713

QY 862 AACTACTATT 872
 |||||
 Best Local Similarity 49.5%; Score 36.4; DB 3; Length 61663;
 Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 QY 615 AGCCCTTGCTTTCAGGAACTTGGAACTGTGGCTGGGGGGATTACCC 674
 |||||
 12938 AGCCCTTGCTAACTCCACAGGCCTCCGCACTTCAGGGATGCCACCTTAATCGG 12879
 QY 675 GCCTTCCCGGTTGTCAGAGCTGTATTGAAGAACMCTAGAGCCGGCGCATGA 734
 |||||
 Db 12878 CTCTCAAGATTTCATAGGAATCTCTTCTGACTCTCAGTAGCTATGGTGA 12819
 QY 735 AACGAAAGCTGTAACAGCCCTTCAATTGGCAATATGAGGATACCAAGGGCC 794
 |||||
 Db 12818 ACTGAGAGTTTGCAAGTCCTAGTATCGTACTCATGGTCAGAATGAAAGTGGC 12759
 QY 795 AGTGTAAACG 804
 Db 12758 AAAGGATTCG 12749

RESULT 13
 US-99-453-702B-62/C
 ; Sequence 62, Application US/09453702B
 ; Patent No. 6365723
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 Burland, Valerie T.
 Plunkett, Guy
 Perna, Nicole T.
 TITLE OF INVENTION: No. 6365723el Sequences of E. coli 0157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch. 1.44MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/453, 702B
 FILING DATE: 03-Dec-1999
 PRIORITY CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 60/110, 955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 REFERENCE/DOCKET NUMBER: 960296.95017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9166
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61663
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 62:
 US-09-453-702B-62

Query Match 3.7%; Score 36.4; DB 3; Length 61663;
 Best Local Similarity 49.5%; Pred. No. 5.7; Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 QY 615 AGCCCTTGCTTTCAGGAACTTGGAACTGTGGCTGGGGGGATTACCC 674
 |||||
 Db 12938 AGCCCTTGCTAACTCCACAGGCCTCCGCACTTCAGGGATGCCACCTTAATCGG 12879
 QY 675 GCCTTCCCGGTTGTCAGAGCTGTATTGAAGAACMCTAGAGCCGGCGCATGA 734
 |||||
 Db 12878 CTCTCAAGATTTCATAGGAATCTCTTCTGACTCTCAGTAGCTATGGTGA 12819
 QY 735 AACGAAAGCTGTAACAGCCCTTCAATTGGCAATATGAGGATACCAAGGGCC 794
 |||||
 Db 12818 ACTGAGAGTTTGCAAGTCCTAGTATCGTACTCATGGTCAGAATGAAAGTGGC 12759
 QY 795 AGTGTAAACG 804
 Db 12758 AAAGGATTCG 12749

RESULT 14
 US-10-114-170-62/C
 ; Sequence 62, Application US/10114170
 ; Patent No. 6855814
 ; GENERAL INFORMATION:
 ; APPLICANT: Blattner, Frederick R.
 Burland, Valerie T.
 Plunkett, Guy
 Welch, Rod
 Perna, Nicole T.
 TITLE OF INVENTION: No. 6855814el Sequences of E. coli 0157
 NUMBER OF SEQUENCES: 265
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Quarles & Brady
 STREET: 1 South Pinckney Street
 CITY: Madison
 STATE: WI
 COUNTRY: US
 ZIP: 53701-2113
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch. 1.44MB storage
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Word Perfect 8.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/10/114, 170
 FILING DATE: 01-APR-2002
 PRIORITY CLASSIFICATION: <Unknown>
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 09/453, 702
 FILING DATE: 03-DEC-1999
 APPLICATION NUMBER: 60/110, 955
 FILING DATE: 04-DEC-1998
 ATTORNEY/AGENT INFORMATION:
 NAME: Seay, Nicholas J.
 REGISTRATION NUMBER: 27386
 REFERENCE/DOCKET NUMBER: 960296.95017
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (608) 251-5000
 TELEFAX: (608) 251-9166
 INFORMATION FOR SEQ ID NO: 62:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 61663
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear
 MOLECULE TYPE: DNA (genomic)
 SEQUENCE DESCRIPTION: SEQ ID NO: 62:
 US-10-114-170-62

Query Match 3.7%; Score 36.4; DB 3; Length 61663;
 Best Local Similarity 49.5%; Pred. No. 5.7; Matches 94; Conservative 0; Mismatches 96; Indels 0; Gaps 0;
 QY 615 AGCCCTTGCTTTCAGGAACTTGGAACTGTGGCTGGGGGGATTACCC 674
 |||||
 Db 12938 AGCCCTTGCTAACTCCACAGGCCTCCGCACTTCAGGGATGCCACCTTAATCGG 12879
 QY 675 GCCTTCCCGGTTGTCAGAGCTGTATTGAAGAACMCTAGAGCCGGCGCATGA 734
 |||||
 Db 12878 CTCTCAAGATTTCATAGGAATCTCTTCTGACTCTCAGTAGCTATGGTGA 12819
 QY 735 AACGAAAGCTGTAACAGCCCTTCAATTGGCAATATGAGGATACCAAGGGCC 794
 |||||
 Db 12818 ACTGAGAGTTTGCAAGTCCTAGTATCGTACTCATGGTCAGAATGAAAGTGGC 12759
 QY 795 AGTGTAAACG 804
 Db 12758 AAAGGATTCG 12749

RESULT 15

US-09-455-486-7/c

Sequence 7, Application US/09455486

Patent No. 6833438

GENERAL INFORMATION:

APPLICANT: Daniel E. Afar

APPLICANT: Rene S. Hubert

APPLICANT: Arthur B. Raiano

APPLICANT: Douglas C. Saffran

APPLICANT: Stephen C. Mitchell

TITLE OF INVENTION: NOVEL SERPENTINE TRANSMEMBRANE ANTIGENS

FILE REFERENCE: 129-17-US-11

CURRENT APPLICATION NUMBER: US/09/455, 486

CURRENT FILING DATE: 1999-12-06

PRIOR APPLICATION NUMBER: 09/323, 873

PRIOR FILING DATE: 1999-06-01

NUMBER OF SEQ ID NOS: 34

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 7

LENGTH: 4429

TYPE: DNA

FEATURE: CDS

ORGANISM: Homo sapiens

NAME/KEY: CDS

LOCATION: (85) ... (1464)

US-09-455-486-7,

Query Match 3.5%; Score 34.4; DB 3; Length 4429;

Best Local Similarity 51.3%; Pred. No. 6.2; Matches 80; Conservative 0; Mismatches 76; Indels 0; Gaps 0;

Qy 243 TATTTCCCGGCTGTGGAGTACCGAAAGATACTGGGAGAATGCCATCGTCACATTGT 302

Db 1726 TCAATCTCAGGCCATGGCTCTGGGAATAATAGACTCAGGGACCTGCATGTGATCTCA 1667

Qy 303 CCCGGATGAGTTGAGACATGGCTGTGCTGCTGAGCTTGGAAAGCGTAAGA 362

Db 1666 CTAACCTGGAGATAAAATGGTGTCTCTCCAGTAGTGCAATTCTCAAGACAAGC 1607

Qy 363 AAAGATTCGATTTAACGATGTTAGAGAAATT 398

Db 1606 ATGTTCCCTCAGTCAGGCTAAGAAACTT 1571

Search completed: March 18, 2006, 11:58:33
Job time : 228 secs

GenCore version 5.1.7
 Copyright (c) 1993 - 2006 Biocceleration Ltd.

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:52:29 ; Search time 992 Seconds

(without alignments)

8302.722 Million cell updates/sec

Title: US-10-812-387-1

Perfect score: 996

Sequence: 1 catatggcacaaggcttac.....atgagcttaattaaggatcc 996

Scoring table: IDENTITY_NUC

Gpop 10.0 , Gapext 1.0

Searched: 9793542 seqs, 4134689005 residues

Total number of hits satisfying chosen parameters: 19587084

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%*

Maximum Match 100%*

Listing first 45 summaries

Database : Published Applications NA Main,*

1: /cgn2_6/podata/1/pubpat/us07_pubcomb.seq: *

2: /cgn2_6/podata/1/pubpat/us08_pubcomb.seq: *

3: /cgn2_6/podata/1/pubpat/us09_pubcomb.seq: *

4: /cgn2_6/podata/1/pubpat/us10_pubcomb.seq: *

5: /cgn2_6/podata/1/pubpat/us10_pubcomb.seq: *

6: /cgn2_6/podata/1/pubpat/us10_pubcomb.seq: *

7: /cgn2_6/podata/1/pubpat/us10_pubcomb.seq: *

8: /cgn2_6/podata/1/pubpat/us10_pubcomb.seq: *

9: /cgn2_6/podata/1/pubpat/us11_pubcomb.seq: *

10: /cgn2_6/podata/1/pubpat/us11_pubcomb.seq: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

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ALIGNMENTS

APOA

RESULT 1
 US-10-812-387-1
 Sequence 1, Application US/10812387
 Publication No. US2005014265A1
 GENERAL INFORMATION:
 APPLICANT: SIVARAMAN, HEPHZIBAH
 PUNDE, ARCHANA VISHNU
 SURBH, CHERAVAKRITU GOPALAN
 APPLICANT: DOBSON, GBORGE GUY
 APPLICANT: BRANNIGAN, JAMES ANTONY
 TITLE OR INVENTION: PROCESS FOR PRODUCTION OF LARGE AMOUNT OF PENICILLIN V
 TITLE OF INVENTION: ACTILASE
 FILE REFERENCE: 058859-0196
 CURRENT APPLICATION NUMBER: US/10/812.387
 CURRENT FILING DATE: 2004-03-30
 PRIOR APPLICATION NUMBER: PCT/IB03/06198
 PRIOR FILING DATE: 2003-12-24
 NUMBER OF SEQ ID NOS: 1
 SOFTWARE: PatentIn Ver. 3.2
 SEQ ID NO 1
 LENGTH: 996
 TYPE: DNA
 ORGANISM: *Bacillus subtilis*
 US-10-812-387-1

Query Match 100.0%; score 996; DB 9%; Length 996;
 Best Local Similarity 100.0%; Pred. No. 1.6e-20; Indels 0; Gaps 0;
 Matches 996; Conservative 0; Mismatches 0;

QY 1 CATATGGCACAAGTCTACATGGAACTGCTGACCTAACATGTTAGCAGACA 60
 Db 1 CATATGGCACAAGTCTACATGGAACTGCTGACCTAACATGTTAGCAGACA 60

QY 61 ATGGATTGTCATTGCTGGGACAGGGTTATCGGTATGGGAGA 180
 Db 61 ATGGATTGTCATTGCTGGGACAGGGTTATCGGTATGGGAGA 180

QY 181 AACCTTGGAAATTATTTGCGGAGGCAATTAAAGCGTTATCTGCGCG 240
 Db 181 AACCTTGGAAATTATTTGCGGAGGCAATTAAAGCGTTATCTGCGCG 240

QY 241 CTTTATTTCCGGGCTATGGGAGTAGAAACGATACGGGAGATACCGTCACATT 300

RESULT 3
US-10-282-122A-9120

; Sequence 9120, Application US/1028212A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A

CURRENT APPLICATION NUMBER: US/10/282,122A

CURRENT FILING DATE: 2003-02-20

PRIOR APPLICATION NUMBER: 60/191,078

PRIOR FILING DATE: 2000-03-21

PRIOR APPLICATION NUMBER: 60/206,848

PRIOR FILING DATE: 2000-05-23

PRIOR APPLICATION NUMBER: 60/207,727

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: 60/230,335

PRIOR FILING DATE: 2000-09-06

PRIOR APPLICATION NUMBER: 60/230,347

PRIOR FILING DATE: 2000-09-09

PRIOR APPLICATION NUMBER: 60/242,578

PRIOR FILING DATE: 2000-10-23

PRIOR APPLICATION NUMBER: 60/253,625

PRIOR FILING DATE: 2000-11-27

PRIOR APPLICATION NUMBER: 60/257,931

PRIOR FILING DATE: 2000-12-22

PRIOR APPLICATION NUMBER: 60/267,636

PRIOR FILING DATE: 2001-02-09

PRIOR APPLICATION NUMBER: 60/269,308

PRIOR FILING DATE: 2001-02-16

remaining Prior Application data removed - See File Wrapper or PALM.

NUMBER OF SEQ ID NOS: 78614

SOFTWARE: PatentIn version 3.1

SEQ ID NO 9120

LENGTH: 984

TYPE: DNA

ORGANISM: Bacillus anthracis

US-10-282-122A-9120

Query Match 28.9%; Score 287.8; DB 7; Length 984;

Best Local Similarity 56.0%; Pred. No. 1.2e-75;

Matches 544; Conservative 0; Mismatches 427; Indels 0; Gaps 0;

Qy 4 ATGTGACAGAGCTTACATGGAACTGCTGAGCTAACATGTTAGCAAGAACATG 63

Db 1 ATGTGACTAGTTGACATTAGAACAAACGGTCAGCATTTTGCAAGAACATG 60

Qy 124 ATGTGACCTGAGGAAGGCCATCAGACAGCTACGGTTATCGGTATGGGAGAAA 183

Db 121 AATATAACGGGTGAAATCAATTAACGAAATGCTACGGTGGGATTTATCAT 180

Qy 184 CTGGAAATATATTTGCGGAGGCATTAATGAAAGCGGTATACGTGCGGCTT 243

Db 181 CGAGGAGGATCATATGCGGAGGACTGAGTATGAGCAGGATGAGATGIGAACCTC 240

RESULT 4
US-10-282-122A-9817

; Sequence 9817, Application US/1028212A

Publication No. US20040029129A1

GENERAL INFORMATION:

APPLICANT: Wang, Liangsu
APPLICANT: Zamudio, Carlos
APPLICANT: Malone, Cheryl
APPLICANT: Haselbeck, Robert
APPLICANT: Ohlsen, Kari
APPLICANT: Zyskind, Judith
APPLICANT: Wall, Daniel
APPLICANT: Trawick, John
APPLICANT: Carr, Grant
APPLICANT: Yamamoto, Robert
APPLICANT: Forsyth, R.
APPLICANT: Xu, H.

TITLE OF INVENTION: Identification of Essential Genes in Microorganisms

FILE REFERENCE: ELITRA 034A

304 CCGCTAGATGTTGAGCATGGCTGTCTGCTGTCAGCTCTTGAGAAGGAAAGAA 363

301 CATTGATTTGTAACTTGAGCTGACAACTCAATCTGCAAGGTTAAGAAA 360

364 AGATTCGATCTAACGATTGAGAGAAATAGTCATATGGATCAGTTACCG 423

361 CTCTGAGATGCAATCACCTTGTGATATACTACATACCGGTTAGGCTTACCCACCA 420

424 CTTCACTGGATATGTCAGACGGACGCCAACCTGAGCTAGAAGCCAGCAC 483

421 CTACATGGATTAGCGATATGGAGATGCTACGTTACGAGTTCACGAGTGA 480

484 GGCTCTAAAGTCTGATATCAGCTGTTGCTATGAGAACAGCCCCACTTATATGG 543

481 GATTAAATTTGTTGATACCCACTAGGAGGTGATGACGATTTCCGGAGTTATGG 540

544 CATTGAACTACGCGACAAATACAGAAATGACGGAACTGAGGAGAC 603

541 CATTACAAATTAGACAAATAATAGCCCTTAATCGCAGCCATCGGCCACAGAG 600

604 ATGGGGGATTAAGCCCTTCTGCTTGGCCCTGGCTAGGACTGTTGCTCTGGGG 663

601 TGGATTAATTACCTTACATTAGTCGTTGGCTTGGCAAGGCTGGCTCAATGGCATTCAGGG 660

664 GATTATAACCCGCTTCCGGTTGAGCTGTTATTGAGAACATCTAGAGCCG 723

661 ATTTCACCCGACATCGAGGTTGTCGGGAGCATGGCAACAAACATTCAGGT 720

724 GCGCCGATGAAACGAAAGTGTACAGCGCGTTCAATTGGAAATATGAGATA 783

721 ATAGATAGGGAGAGAGGGATATCAGCCCTTTCTATCTATCATATGAGGTT 780

784 CAAAGGGCGCTGATAAGGAGAGAGGAAATCATATAAGGAAATACTCCGG 843

781 CTCAAAGGGTGGATTAATACAGAAAGAGGTGTCATTAGATAACCATATACAGGTA 840

844 ATGTGCAAGGAAACTGAAACTACTATTCACCACTATGACAATGGAAATCCAAAAA 903

841 ATGGTAGGAACTGGAAATTTATCATCTACTTACGATGTTGAGAAATTTAGCT 900

Db 904 GTAAATTATTCATGAGACCTGACTGTTGGCTTAAGGTGTTGGCTAAAGCA 963

Db 901 GTTCATTATTCATGAAATTAGATACAGATGAGTAAAGCTATCGTCCACGG 960

Qy 964 GANGAGACTAT 974

Db 961 AACACAAAT 971

CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-01-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PAlM.

SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 9817
 LENGTH: 969
 TYPE: DNA
 ORGANISM: *Bacillus anthracis*

US-10-282-1228-9817

Query Match 23.8%; Score 237; DB 7; Length 969;
 Best Local Similarity 55%; Pred. No. 2.5e-60;
 Matches 538; Conservative 0; Mismatches 425; Indels 6; Gaps 4;

QY 4 ATGTGSCACAMGTCTTACATGGAACTGTCTAACCGTAACTGTATTAGCAAGAACATG
 1 ATGTGACTAGTTGACATTGAGACAAACACGGTCAGCTCTTGGAGAGATG 63
 Db 64 GATTGTCATTTCAGCTGGGACAGGGTATTGCTACCGTAACTGTATTAGCAAGAACATG
 1 ATATATACGSGTGAAATCATTAATGAAAGATGCTACGGTGGATGGATTATCAT 123
 Db 61 GACTTCACATTAGATGAACTGAGATAATATTCTCGACATTACAGTGAAAT 120
 124 ATGTGAGCTGAGGAAGGCCATCAGACAGTAGCCGTATTGGTATGGAGAAA 183
 121 ATATATACGSGTGAAATCATTAATGAAAGATGCTACGGTGGATGGATTATCAT 180
 QY 184 CTGGAAATATATTATGCGGACGGCATTATGAAAGCGGTTATCTGGGGGCTT 243
 181 CAAGGAGGATCATATGGCGACGGGTAATGAAACGGATGACATGCAACACTC 240
 Db 244 TATTTCGGGCTATCGGAAAGATCGGGAGATCGGTACATGTC 303
 Qy 241 TATTTCGGGCTATCGGAAAGATCGGGAGATCGGTACATGTC 300
 Db 304 CGCGCATGTTGACATGGCTCTCACTCTGTCACTT-GGAAGACGAAAG 361
 301 CGATTGATTGTTGAACTGGAGCTGACAAATTATCTGCAAGACGAGAAGA 360
 Qy 362 AAAGATTCGCTCTTAACTGATGAAATAATGATCTATGGATCACITTA 420
 361 ATCTGTAGATGACATTACCTTTGGATATACATACCGGATTAGACTTGC 420
 Db 421 CGCGCTCACTGATGAACTGCAACCGACGCGCGAACCTGACATGAAAGCA 480
 421 CGCACTACATTGATGAACTGCAACCGGATTAATGGGAGATGCTGACAGT 480
 Db 481 GAGGGCTCAAGTCATGATACAACTGTCATGAGAACGCCCGACTTATA 540
 481 GRAGGTTAAATGTGTGATACCACTAGGGTGTGAGGAAATGCTCCGAGTTAAT 540
 Qy 541 TGGCATGAACTCGGAAATACAGGAATCAGACGAACTGAGGAGAGAGCAA 600
 Db 541 TGGCATTACAAATTAGACGAAATATAGCCCTAAATCCGACCATGGGCCACA 600

RESULT 5
 US-10-398-221-766
 Sequence 766, Application US/0398221
 Publication No. US20040018514A1
 GENERAL INFORMATION:

APPLICANT: KUNST, Frederik
 TITLE OF INVENTION: Listeria innocua, genome and applications

FILE REFERENCE: 344 702 - US
 CURRENT APPLICATION NUMBER: US10/398,221
 CURRENT FILING DATE: 2003-03-27
 PRIOR APPLICATION NUMBER: PCT/FR 01/03 061

PRIOR FILING DATE: 2001-10-04
 PRIOR APPLICATION NUMBER: FR 00/12 697

PRIOR FILING DATE: 2000-10-04
 NUMBER OF SEQ ID NOS: 4025

SOFTWARE: PatentIn version 3.0.
 SEQ ID NO: 766
 LENGTH: 990
 TYPE: DNA
 ORGANISM: *Listeria monocytogenes*-EGD

US-10-398-221-766

Query Match 23.4%; Score 232.6; DB 7; Length 990;
 Best Local Similarity 53.0%; Pred. No. 5.5e-59;
 Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;

QY 4 ATGTGACAGCTCTTACATGGAACTGTCTAACATGTTATGGAGAACATG
 1 ATGTGACAGCTCTTACATGGAACTGTCTAACATGTTATGGAGAACATG 63
 Db 64 GATTGTCATTGAGGAGAGGGGTTATGGCTACGGCTAACATGTTATGGAGAACATG 60
 61 GATTGTCATTGAGGAGAGGGGTTATGGCTACGGCTAACATGTTATGGAGAACATG 120
 Qy 124 ATGTGAGCTGAGGAAGGCCATCAGACAGTAGCCGTATTGGAGAAA 183
 121 TCTTCACAGCGGGCCATTATTAATGATCTGATGTTGGAGGGAGAGAG 180
 Qy 184 CTGGAAATATATTATGCGGACGGATTATGAAAGAGCGGTTATCTGGGGCCTT 243
 181 TTGATAATAACATTGAGGAGGATGAGGAGGATGAGGAGGATGCTGACCTA 240

QY 244 TATTTCCGGGCTATCGGGAGTACGAAAACGATACGGGAGATACCGTCACITGTC 303
Db 241 TATCTTCAGGAGAACGAGCACTTATGCCGCAGCAGGTGAGGAAATCAATTAGCT 300
QY 304 CGCATGAGTTGTGACATCGGGCTGTCAGCTGTCAGTTGGAGAGCTTAAGAGA 363
Db 301 CCACAGAGATTTCAGATTTGCTGTTAGGACTTGCGAACGATTAAGATGGAAGA 360
QY 364 AAGATTGAGTTAACGATTTGAGTAGAAATAATAGATTTATGATAGATAGTTACGG 423
Db 361 AAGTTATCGGTTATACCTTGTGGATCACACCAGTACCGTTACTTGGAATCACACCA 420
QY 424 CTTCACTGGATATTCGAGCGACGGCGAACCTGAGATAGAACCGAGCACAGAC 483
Db 421 TTACACTGGATTTCAGAGAACGAGTGTGGCTGTTAGTGAACCRACAGAAACA 480
QY 484 GGCTTCAAGCTATGATATCAACACTGGTGTATGACGAGACAGCCCGACTTATGG 543
Db 481 TCGCTTCGTTAAAGAACCCCTGAGGTTATGACAAATGCCACCCATGAAATGG 540
QY 544 CATTGAAACCATCTTCAGGATATACAGGATACACCGAGCTTACGGAGAACAGG 603
Db 541 CATATCGAGATTACGCAACTACAGGTTACAGCACAGTTACAGCACACATTAGGG 600
QY 604 ATGGCGGGATTAGCCCTTCTGCTTTGGCAAGGCTTGGAACTGTTGCTCCGGGG 663
Db 601 TTGGAGAGATATGCTAAACCATTTCTCAAGGAGAACGAAATTACCGAT 660
QY 664 GATTATACGCGCTTCCGGTTCTCAGGCTTTCAATTGGCAATATACGAGA 723
Db 661 GTTATTAATCGGAGAACGGAGGTTACAGGGCTTTCAATTGGCAATATACGAGA 720
QY 724 GCGCCGCGATTAACGAAAGGTGTTACAGGGCTTTCAATTGGCAATATACGAGA 783
Db 721 GCGAAACACAGAGAACGGAGGTTACAAATGTTGTTGAAAGAACATTTATGAA 780
QY 784 CCAAAGGGCGCAGTGAATAACGGAAGAACGAAATCTATAGCCTATACCTCCGG 843
Db 781 CCGATGCGAGGTTAAAGAACGTTGCTGACCTGTATTCACAAATATGCGATCT 840
QY 844 ATGGCAACGAACTGGAACTACTATTCACCACTATCACAACTGGCAATCAAA 903
Db 841 ATGGTTCCGGAAGCAAAAGTCACTTACCTCATAGGAAACAAACCAATCAATG 900
QY 904 GTAAATTATTCATGAGAACGACTTGACTGTGTTGGA 938
Db 901 GTTACTTGCTGAGAACGTTATAGAAATATGAA 935

RESULT 6
US-10-398-221-2682

; Sequence 2682, Application US/10398221
; Publication No. US20040018514A1
; GENERAL INFORMATION:
; APPLICANT: KUNST, Frederik
; APPLICANT: GLASER, Philippe
; TITLE OF INVENTION: Listeria innocua, genome and applications
; FILE REFERENCE: 344 702 - US
; CURRENT APPLICATION NUMBER: US/10/398,221
; CURRENT FILING DATE: 2003-03-27
; PRIORITY APPLICATION NUMBER: PCT/FR 01/03 061
; PRIORITY FILING DATE: 2001-10-04
; PRIORITY APPLICATION NUMBER: FR 00/12 697
; PRIORITY FILING DATE: 2000-10-04
; NUMBER OF SEQ ID NOS: 4025
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 2682
; LENGTH: 990
; TYPE: DNA
; ORGANISM: Listeria monocytogenes EGDe
; US-10-398-221-2682

RESULT 7
US-10-282-122A-24755
; Sequence 24755, Application US/10282122A
; Publication No. US20040029129A1
; GENERAL INFORMATION:

Best Local Similarity 53.0%; Pred. No. 5.56-59; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;
Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;
QY 4 ATGGCCACAGCTTACATGGAACTGCTGACGGTAACTGATGTTAGGAGAAATG 63
Db 1 ATGGCCACAGCTTACATGGAACTGCTGACGGTAACTGATGTTAGGAGAAATG 60
QY 64 GATTGCGATTTGAGCTGGGGAGAGGGTATCTCTATOCGCGCCGTTACAGCTGGAAC 123
Db 61 GATTGCGATTTGAGGGCAACCAAACTAGCCAAAGAAATTAGGATGGGAA 120
QY 124 ATGGAGCTGACGGRAGGCCCTACGACRCACTGACGCTTATCGTAAGGGAGAAA 183
Db 121 TCTTCTACAGACGGGCTTAAATTATATAGATGATGCAATTGTCGAGGGAGAG 180
QY 184 CTGGAAATAATATATTGCGAGGGATAATGAAAGGGTTATCTTGCGGGCTT 243
Db 181 TTGATTAATACATTTCAGAGGTTAGTGAATGAGAGGATTAAGCTGTCATCTA 240
QY 244 TATTTCGGGTTATGCGAGGAGAACGATAACGGAATATCCCTCACATTGTC 303
Db 241 TATCTTCAGGAGAACGTTATGCCAGCACCGTACGGTGAAGGAAATCAATTAGCT 300
QY 304 CCGCGTGGATTCAGGGGCTGTCAGCTGTCAGCTGCTTGGAGAGCTTAAGGAA 363
Db 301 CCACAGAAATTTCGCTTACGCAACGAAATGTCGAGATGCAACGATTAAGCTGTC 360
QY 364 AAGATTGAGCTTTAACGTTGAGGAAATAATGATCTATGGATACAGTTACCC 423
Db 361 AAGTTATCGTTAACGTTGCTGATGACCTGTTACCGTACTGTTACAGCTACCCA 420
QY 424 CTTCACTGGATATGTCAGACGGACGGCCGAAACCTACGATAGAACAGGAGAC 483
Db 421 TTACACTGGATTTCACAGAACGAGACGGCTGTTGTTAGTGAACCAACAGAA 480
QY 484 GGCTCAAGTGTGTTGATCACCTGGTGTGTTGAGGACGCCCCACTTTATGG 543
Db 481 TCGCTTCGTTAAAGAACAAACCTGTTGAGGTTATGCAATAGCCACGATGATGG 540
QY 544 CATTGAAACCATCTTCAGGAACTATACGAAATAGCAAGGAAATAGGCAAAAGG 603
Db 541 CATATCGAGATTACGAACTACACGAACTTACAGGTTACAGAACACATTTAGGG 600
QY 604 ATGGCGGGATTAGCCCTTCTGTTGGCAAGGCTTGGAACTGTTGTCGCGGG 663
Db 601 TTGGAGAGTATGGCTAACCAATTGCGTACGGTACAGGACAAATTACCGAT 660
QY 664 GATTATACGCGCTTCCGGTTGGAGGTTGGTTGAGAACATCTGGCCCG 723
Db 661 GTTATTAATCGGAGAACGAGCTTGTGTCGCGCACACTTGAAAGAAATATGAA 720
QY 724 CCAAAGGGCGCAGTGAACGGAAGAACGAAATCTATGCTGCGCTTCAATTGCGAATATGAC 783
Db 721 GCGAAACAGGAGAACGAGCTTACACAAATGTTGCGATGTCGCGCAGT 780
QY 784 CCAAAGGGCGCAGTGAACGGAAGAACGAAATCTTACGCAATATCTCCGG 843
Db 781 CCGATGCGAGGTTAAAGAACGTTGCTGACCTGTATTCACAAATATGCGATCT 840
QY 844 ATGGCAACGAACTGGAACTACTATTCACCACTATCACAACTGGCAATCAAA 903
Db 841 ATGGTTCCGGAAGCAAAAGTCACTTACCTCATAGGAAACAAACCAATCAATG 900
QY 904 GTAAATTATTCATGAGAACGACTGTGTTGGA 938
Db 901 GTTACTTGCTGAGAACGTTATAGAAATATGAA 935

Query Match 23.4%; Score 232.6; DB 7; Length 990;

APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlsen, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Trawick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forrester, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELITRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/205,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 24755
 LENGTH: 990
 TYPE: DNA
 ORGANISM: Listeria monocytogenes
 US-10-282-122A-24755

Query Match Best Local Similarity 23.4%; Score 232.6; DB 7; Length 990; Matches 496; Conservative 0; Mismatches 439; Indels 0; Gaps 0;
 QY 4 ATGTGACAGTGTCTACATTGGAACTCTGACCGTAAACATGATATTGGACAGACATG 63
 Db 1 ATGTGACAGTGTCTGATTAGAAACCTGTTAGGAAACATTATTCAGAACATG 60
 Qy 64 GATTATAACCGCCTTCCCGGTTGCTAGCTGGTATTGAAGAACATCTAGAG 723
 Db 61 GGTATATCTGCCAGAACCTTGCCCTGGCCATACTTGAAATATTTAA 720
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 24755

RESULT 8
 US-10-429-802-17
 ; Sequence 17, Application US/10/429802
 ; Publication No. US20030228285A1
 ; GENERAL INFORMATION:
 ; APPLICANT: HUNG, MIEN-CHIE
 ; APPLICANT: WONG, KA YIN
 ; APPLICANT: ZOU, YI-YU
 TITLE OF INVENTION: BI-PARTITE T-CELL FACTOR (TCP) - RESPONSIVE PROMOTER
 FILE REFERENCE: USC:752US
 CURRENT APPLICATION NUMBER: US/10/429, 802
 CURRENT FILING DATE: 2003-05-05
 PRIOR FILING DATE: 2002-05-03
 NUMBER OF SEQ ID NOS: 54
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO: 17
 LENGTH: 1616
 TYPE: DNA
 ORGANISM: Bacillus sphaericus
 US-10-429-802-17

Query Match Best Local Similarity 17.4%; Score 173.8; DB 6; Length 1616; Matches 495; Conservative 49.8%; Pred. No. 4.1e-41%; Mismatches 492; Indels 6; Gaps 2;
 Qy 7 TGCACAGTCTACATGGAAACTGTGGCAATGTTAGGAAACATGAT 66
 Db 335 TGCAGTAGCTTATCAATCTGTAACAGCATGATATAAATTCGCTGCACATGAT 394
 301 CCACAAAGATTTGCTTGTGACTTGCGAACGATTAAAGATGGAGCA 360
 Qy 67 TTGCAATTCACTGGACAGAGGTCTCTACCGCCCGTACAGCTGGAAACAGT 126

Page 7

395 TTACATGGACCAGATAGTAAAGTATTGTCCACCGTAATTACGCCATCGATT 454
 127 GAGCTGACGGAA- - GGGCCCATCAGACACGTACCGTTATCGGTATGGAGA- - 181
 455 TTAGAAAAGGAATGTAGTCATTACAAATCTATGCTTGTGGATGGAGAAC 514
 182 -ACTTGAAATATATTATTGCGACGGCATTAATGAAAGGGTTATCTGTGCGCG 240
 515 GACATTACATCACCAGTCTCATGATGAGGGTAACGAAAGGATTAAATGGGCCATG 574

; TITLE OF INVENTION: TARGETING PROTEINS TO
; TITLE OF INVENTION: REAGENTS
; FILE REFERENCE: UTSC-797US
; CURRENT APPLICATION NUMBER: US/10/430,500
; CURRENT FILING DATE: 2003-05-06
; PRIORITY APPLICATION NUMBER: 60/383,063
; PRIORITY FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
SPO TN NO :

RESULT 10
 Sequence 34300, Application US/10028122A
 Publication No. US200401029129A1
 GENERAL INFORMATION:
 APPLICANT: Wang, Liangsu
 APPLICANT: Zamudio, Carlos
 APPLICANT: Malone, Cheryl
 APPLICANT: Haselbeck, Robert
 APPLICANT: Ohlson, Kari
 APPLICANT: Zyskind, Judith
 APPLICANT: Wall, Daniel
 APPLICANT: Travick, John
 APPLICANT: Carr, Grant
 APPLICANT: Yamamoto, Robert
 APPLICANT: Forseyth, R.
 APPLICANT: Xu, H.
 TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 FILE REFERENCE: ELTRA_034A
 CURRENT APPLICATION NUMBER: US/10/282,122A
 CURRENT FILING DATE: 2003-02-20
 PRIOR APPLICATION NUMBER: 60/191,078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/206,848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207,727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/230,335
 PRIOR FILING DATE: 2000-09-06
 PRIOR APPLICATION NUMBER: 60/230,347
 PRIOR FILING DATE: 2000-09-09
 PRIOR APPLICATION NUMBER: 60/242,578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253,625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257,931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/267,636
 PRIOR FILING DATE: 2001-02-09
 PRIOR APPLICATION NUMBER: 60/269,308
 PRIOR FILING DATE: 2001-02-16
 Remaining Prior Application data removed - See File Wrapper or PALM.
 NUMBER OF SEQ ID NOS: 78614
 SOFTWARE: Patentin version 3.1
 SEQ ID NO: 34300
 LENGTH: 978
 TYPE: DNA
 -ORGANISM: *Staphylococcus epidermidis*
 US-10-282-122A-34300

Query Match: 16.1%; Score: 160.2; DB: 7; Length: 978;
 Best Local Similarity: 49.9%; Pred. No: 4e-37; Matches: 458; Conservative: 0; Mismatches: 453; Indels: 6; Gaps: 2;

RESULT 11
 US-10-724-972A-1455
 Sequence 1455, Application US/10724972A
 Publication No. US2004014773A1
 GENERAL INFORMATION:
 APPLICANT: Doucette-Stamm, Lynn
 APPLICANT: Bush, David
 TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS
 TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
 FILE REFERENCE: PATH03-16
 CURRENT APPLICATION NUMBER: US/10/724,972A
 CURRENT FILING DATE: 2003-12-01

Db 1115 ATCCCCAAAAGGGTGTGTTGACAATGAGGGAAACGGATTACCACTTACCTCA 1174
 Qy 841 GTGATGTGCAAGGAACCTGAACTACTATTCACCACATGACAATCGAACATCCA 900
 Db 1175 GCTATGTGCGCACAAAGTAACATTAACTTAAACTGTGAACTGTTAGTGATGTTCA 1234
 Qy 901 AAAGTAATTTATTCATGAGACCTGACTGTTGGAGCTTAAGTGTTCGCTAA 960
 Db 1235 GCGGTTCCTTAACTGCTGAAATTAAATAGTCAGATTAACTCATTTAGGGAT 1294
 Qy 961 GCAGAGAGAGTATCAGTGAAGTTATTAGGA 993
 Db 1295 CGTAAKCAAGATAATTAAAGCATTAACTCAGTA 1327

Db 64 GATTTGCATTCTACGGACAGAGGTCTCTTCAGCGCCGTTACAGCTGGAC 123
 Qy 61 GACTTGTGATTGATTATGTTATCCAAACATTGTTCCACGTCTATCCTACCAA 120
 Db 124 AGTGTAGGTGACGGAAAGGCCCTACAGACAGCTACGGTTATCGGTATGGGAGA 183
 Qy 121 TTGATCTAGATCA--GACATCGCTTGAAATGCTTGTGACAATTAA 177
 Db 184 CTTGAAATATTTGCGACGGCTTAATGAAACGGTTATCTGTGGCGGTT 243
 Qy 178 GTAGGACCTATGATGTTGTGATGGTTAAKGAAAGGTTAGCTATTGCAACCT 237
 Db 244 TATTTCGGCTATGGAGTAGAAAGACATCGGAGATACCGTCATTC 303
 Qy 304 CCGCATGAGTTGACAGGGCTCTGTCAGTCGTGTCGTCGTTGGAAAGCTAA 363
 Db 298 CCTGAGGAGTTGTTGGTTAGCTTAAAGTATGAGAAATTAAGCA 357
 Qy 364 AAGATCCTCTTAACTGAGAGAAATTAGATCTATGGATACAGTTACCG 423
 Db 418 TTACATTCTGGTCACTGTGAAACAGACATACCGCTACGCAATGC 477
 Qy 358 AAGGTTAAGAGTCATATTGATGAAAMATACTTGAACTTGAATCTCT 417
 Db 424 CTGACTGATGTTGACGGAGCGGGCTCTGTCAGTCGTGTCGTTGG 483
 Qy 544 CATGAAACATCTGCAACATACAGAACTGACCCGAAAGCTGGAGAAC 603
 Db 538 CATCTATCTACTTAAGAAATTGCTTAAACACCAACAGAAATCACCATA 597
 *
 Qy 604 ATGGCGGATTAGCCCTCTGCTTGTGCAAGGCTTAGGAACTGTGTCTCCGGG 663
 Db 598 ATAGGTAATGCTGTTAGATCATGCTGGTTGAAAGCAGGAAATGGCTTACGGGT 657
 Qy 664 GATTTACACGGCTTCCGGTTGTCAGGCTCTTATTGAAAGAATCTGAGCC 723
 Db 658 GGTTATCTACGCAAGCTTACGGCTACATTTAGACCACTACGGCT 717
 Qy 724 GCGGCGATGAAACGAAAGGTGACGGCTTCAATTGGCAATATGAGATA 783
 Db 718 TCCCATATGAGATGAAATTATGTTAAGTCTGAGTCAGTCAGTATC 777
 Qy 784 CCAAGGGCCAGTGTAAAGGAAGAACGAAATTCTTATGCCATTACTTCGGT 843
 Db 778 CCTCAGGGCGATTAACTGCAATTAATACATACACATATCAATTAGTG 834
 Qy 844 ATGCGCAACGAAACTGGAACACTATTCACCATCTGACAACTCGGAAATCAA 903
 Db 835 ATGGAGATGAAAGAAAGCTTAAGCCATCTTAACTCAATTTC 894
 Qy 904 GTAAATTATTCATGA 920
 Db 895 ATAAATTAACTGAGA 911

Query Match 16.0%; Score 159; DB 7; Length 995;
 Best Local Similarity 49.8%; Pred. No. 9.2e-37; Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Qy 2 ATATGTCACGAGCTTACATTTGGAAACTGCGTAACATGATGAGCAAGACAA 61
 Db 14 ATATGTCACGAGCTTACATTTGGAAACTGCGTAACATGATGAGCAAGACAA 73

Qy 62 TGGAGTTGGATTAGCTGGAGCAGAGGTGATTCCTCTCCGCCCTACAGCTGA 133
 Db 74 TGGAGTTGGATTAGCTGGAGCAGAGGTGATTCCTCTCCGCCCTACAGCTGA 73

Qy 122 ACAGTTGCAAGCTGAGGAAGGCCCATCAGCACAGTACCGTTATCGTATGGGAGA 181
 Db 134 AATTTGATCAGATTCAGACATGGCTT--GAATATGGTTTGTGACAATTTAA 190

Qy 182 AACCTGGAAATAATATTGGCGACGGCTTAATGAAGCGGTATCTGTGGGCC 241
 Db 191 AAGGAGGACCTTATGATGTTGGTGTGTTAACGAAAGGTGTAGTTTGAAAC 250

Qy 242 TTATTTGGGTATGGCGAGAGAAAACATACGGAGATACGGTACATGGTACATG 301
 Db 251 ATTACTTCACTGGTGTGACRTGGGGCTCTCAGCTGTGCTTGTGAGGTTAAG 310

Qy 302 TCCGGATGTTGGTGTGACRTGGGGCTCTCAGCTGTGCTTGTGAGGTTAAG 361
 Db 311 CACCTGAGGGTTATGGTTGGTTAATAAGATTTAGGAAATTAAAC 370

Qy 362 AAAGATTCGATCTAACCTTGTAGAGAAATTAGACCTATGGATACGTTCAC 421
 Db 371 AAAAGGTTAGAAATCAATATTAGATGAACTAAATGGACTTC 430

Qy 422 CGCTTCACTGGATTTGTGAGGACGGCGGAAACCTGACATAGAACAGAGCG 481
 Db 431 CTTCACATTCTGTCACGTGATGAAACGGACATACCGTAGCCATAGCTCACATG 490

Qy 482 ACGGCCTCAAGCTPATGATAACCTGGTGTGACGACAGCCGCACITATAT 541
 Db 491 GCTTAAATAGTTAGAATATTGATCACTTAAACAGAACCTTAATTAGATT 550

Qy 542 GGCGATGAACTGACCGATTTGCGGTTCTGGCCAGGGCTAGGACTGTTGGCTCG 601
 Db 551 GCGATCTATCTACTTAAGAAATTACGCTTTAACCCACAGAACTCAACCAT 610

Qy 602 AGATGGGGCGATTAACCTGAGGAACTTACAGGAATCTAGAGCAAG 661
 Db 611 TAATAGTTAGCTTGTAGAATCACTGGCTGTGAGGAGAACATTGGTTACCG 670

Qy 662 GGGATTAATACCGCCCTTCCGGTTGTGAGGCTGTATTGAAAGAACATCTAGAC 721
 Db 671 GGGGTATAGCTGACAGATGTGTTATAGCGCTACATTTAGACACCACTACGT 730

Qy 722 CGCGGGCGATGAAAGGCTAACAGCGCTTCAATTGTGCAATATGAGCA 781
 Db 731 GTTCCATATGAAATTATGATGAAATTATGATGTTTGTGAGCTGATGTCAGTC 790

Qy 782 TACCAAGGGGAGTACCGAGAGAACGAAATTATAGGAAATACTCCG 841

; TYPE: DNA
 ; ORGANISM: S.epidermidis
 ; US-10-724-972A-1455

RESULT 12
 US-10-282-122A-7960
 ; Sequence 7960, Application US/10282122A
 ; Publication No. US20040029129A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Liangsu
 ; APPLICANT: Zamudio, Carlos
 ; APPLICANT: Malone, Cheryl
 ; APPLICANT: Haselbeck, Robert
 ; APPLICANT: Ohlsen, Kari
 ; APPLICANT: Zyskind, Judith
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Trawick, John
 ; APPLICANT: Carr, Grant
 ; APPLICANT: Yamamoto, Robert
 ; APPLICANT: Forsyth, R.
 ; APPLICANT: Xu, H.
 ; TITLE OF INVENTION: Identification of Essential Genes in Microorganisms
 ; FILE REFERENCE: ELITRA_034A
 ; CURRENT APPLICATION NUMBER: US/10/282-122A
 ; PRIOR FILING DATE: 2003-02-20
 ; PRIOR APPLICATION NUMBER: 60/191,078
 ; PRIOR FILING DATE: 2000-03-21
 ; PRIOR APPLICATION NUMBER: 60/206,848
 ; PRIOR FILING DATE: 2000-05-23
 ; PRIOR APPLICATION NUMBER: 60/207,727
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: 60/230,335
 ; PRIOR FILING DATE: 2000-09-05
 ; PRIOR APPLICATION NUMBER: 60/230,347
 ; PRIOR FILING DATE: 2000-09-09
 ; PRIOR APPLICATION NUMBER: 60/242,578
 ; PRIOR FILING DATE: 2000-10-23
 ; PRIOR APPLICATION NUMBER: 60/253,625
 ; PRIOR FILING DATE: 2000-11-27
 ; PRIOR APPLICATION NUMBER: 60/257,931
 ; PRIOR FILING DATE: 2000-12-22
 ; PRIOR APPLICATION NUMBER: 60/267,636
 ; PRIOR FILING DATE: 2001-02-09
 ; PRIOR APPLICATION NUMBER: 60/269,308
 ; PRIOR FILING DATE: 2001-02-16
 ; Remaining Prior Application data removed - see File Wrapper or PALM.
 ; NUMBER OF SEQ ID NOS: 78614
 ; SEQ ID NO 7960
 ; LENGTH: 993
 ; TYPE: DNA
 ; ORGANISM: Staphylococcus aureus
 ; US-10-282-122A-7960

Query Match 14.7%; Score 146; DB 7; Length 993;
 Best Local Similarity 47.5%; Pred. No. 7.7e-33; Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

Qy 4 ATGGCAAGGTTATGGAAACTGCTGCGAACATGATGAGCAAGACATG 63
 Db 1 ATGGCAAGGTTACGATCAACTTAATGAGCTCTGGAGGACCGATG 60

Qy 64 GATTTCGATTCGCTGGGGACAGAGTGTGATCTCTGGAC 123
 Db 61 GATTATGATTTGATTAGATGTTGGCTCCGAGCTGAGGCTAGAAATATGCTGAC 120

RESULT 13

US-08-781-986A-44/C
 Sequence 444, Application US/08791986A
 Publication No. US20030105446A1

GENERAL INFORMATION:
 APPLICANT: Charles Kunisch
 TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences
 NUMBER OF SEQUENCES: 5255
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Human Genome Sciences, Inc.
 STREET: 9410 Key West Avenue
 CITY: Rockville

Qy 124 ATGGAAGCTGACGAAAGGCCCATCAGACACAGTACSGGTATCGGTATGGAGAAA 183
 Db 121 TCTCGCACT--GGCACGACGCCAACGCAATTGGCTTATGGTACAGAACAGT 177

Qy 184 CTGGAATAATATATTGCGGCGGATTAAACGGTTATCTGGCGGCGT 243
 Db 178 ATGGAAAGTTTATTTAGTGCGGTGTTAGTGCAGTCAGTGGGTGTT 237

Qy 244 TATTTCGCGGCTAAGCGGAGTAGGAAGAACGATACGGGATACGGTACATGTC 303
 Db 238 TATTCCGAGTTAGTCATAGTCATAGTCGTCAGACAGAACAGCGGAGCTAAG 297

Qy 364 AGATTCGATCTTACGATTGAGAAATTAGACTATGGATACAGTTACCG 423
 Db 358 CAAAGCATCCAAATACATGTTGAGGTTATTAATGACATGGTACAGTGGCA 417

Qy 424 CTTCACTGGGATATGTCAGACGGAGGGCGGAAACCTGACGATAGAACAGGAC 483
 Db 478 GAAAGTGGTATAAAGATAACCTTATGGGTCTAACAAATCATCCAGACTAGATGG 537

Qy 544 CATGAAACCATCTCGAGCAATAACAGGATACAGCAGACGAGCAATTAGAGGAG 603
 Db 538 CATTATGTTAATTAAGACATATAATTCTCTTATCCAGCAACAGCAAGTTA 597

Qy 604 ATGGGGGATTAGCCCTTCGCTTGGGAGCTTAGGAACTGTTGGCTCGCGGG 663
 Db 598 TGAGGAGGTTAACCTTAAAGATAACCTTATGGGTCTAACAAATCATCCAGACTAGATGG 657

Qy 664 GATTATAACCGCCCTTCGCGTTGTCAGAGCTTATTGAGACATCTAGAGCG 723
 Db 658 GATTACTTCACTGAGCGCTTGTGAGAAAGCAGAACATGCTCAA 717

Qy 724 GGGCGGATGAAACCAAGGTAAACAGCGCTTCAAAATTGCAAAATATGAGATA 783
 Db 718 AACATGATGATAAGAAATTGATTAAATGATGCAATTATTATAGATGGGTAAATA 777

Qy 784 CCAAGGGCGGAGTGAACCGGAGAACATTCAATTACCAATTACTTCGTT 843
 Db 778 CGGATGGTAACTGTCGCGCATATGTCACATTACATTACATTGTTACGCGTA 837

Qy 844 ATGTCACAGGAACTACTATTCCACCATATGCAATGGCAATCCAAAAA 903
 Db 838 ATAATTAACCTACAGAACCTTATATTAGTATATGCGAGATAGTAGCA 897

Qy 904 GTAAATTATTCATGAGACCTTGTACTGTGGCCTAAAGTGTTCGCTAAAGCA 963
 Db 898 TTAAGCTCAGAGATTATTAGAAGATATGAGCATTTAACCTGAGAG 957

Qy 964 GRAGAGAGTACATGAGCTTATTAGAAGTGTGAGAAATTAGACTATGGATACAGTTACCG 989
 Db 958 CATATGCTATGAGTGTGAGTGA 983

STATE: Maryland
 COUNTRY: USA
 ZIP: 20850

COMPUTER READABLE FORM:
 COMPUTER: HP Vectra 486/33
 OPERATING SYSTEM: MSDOS version 6.2
 SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/781,986A
 FILING DATE:
 CLASSIFICATION: 435
 PRIOR APPLICATION DATA:
 REFERENCE/DOCKET NUMBER: PBZ48PP

TELECOMMUNICATION INFORMATION:
 TELEPHONE: (301) 309-8512
 TELEFAX: (301) 309-8504

ATTORNEY/AGENT INFORMATION:
 NAME: Benson, Bob
 REGISTRATION NUMBER: 30,446
 REFERENCE/DOCKET NUMBER: PBZ48PP

SEQUENCE CHARACTERISTICS:
 LENGTH: 11466 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: double
 TOPOLOGY: linear

US-08-781-986A-444

Query Match Score 14.7%; Length 11466;
 Best Local Similarity 47.5%; Pred. No. 2.9e-32;
 Matches 468; Conservative 0; Mismatches 515; Indels 3; Gaps 1;

Qy 4 ATGTCACAGGTTACATGACTTAACTTAATCATGACTCTTCGACCGAACATG 63
 Db 3688 ATGTCACAGGATCAACATCACTTAATCATGACTCTTCGACCGACGAG 3629

Qy 64 GATTGCGATTCAGTCGGGAGAGGGTATCTCTAACCGCCGTTACAGTGGAC 123
 Db 3628 GATTATGTTATCCATTAGATGGTTCGGCAGCAGTGGACAGGACAGAT 3569

Qy 124 ATGGAAGCTGACGAAAGGCCCATCAGACACAGTACSGGTATCGGTATGGAGAAA 183
 Db 3568 TCTTCGCACT--GGCACGACGCCAACAGCAATATGGCTTATGGACAGGACAT 3512

Qy 184 CTGGAATAATATATTGCGGAGCTTAAGAACGGTTATCTCTGGCGCTT 243
 Db 3511 ATGGAAAGTTTATTTAGTGAGGTTAATGACATGGCAATTCACACAA 3452

Qy 244 TATTTCGCGGCTAAGCGGAGTAGGAAGAACGATACGGGAGTACCGTCATGTC 303
 Db 3451 TATTCCGAGTTAGTCATAGTCATAGTCAGACACAAAGCGGAGCGCATGAAATTAG 3392

Qy 304 CGCGATGAGTTGAGACGGGCTGTGAGCTTGGGATATACACAGCATGAGATGAA 363
 Db 3391 CAAATGAAATTGTCACATGGATTGGGATATACACAGCATGAGATGAA 3332

Qy 364 AGATTCGATCTTACGATTGAGAAATTAGACTATGGATACAGTTACCG 423
 Db 3331 CAAAGCATCCAAATACATGTTGAGTGTATTAATGACATCGGTGAAGTTCGCCA 3272

Qy 424 CTTCACTGGGATATGTCAGACGGAGGGCGAACCTGACGATAGAACAGGAG 483
 Db 3271 TGTGATTATGATGTTTCGCGACTGCACTGCAATCATCCAGACTTAATGG 3212

Qy 484 GGCTCAACTCTGTTACCTGGGCTGTGAGACAGCGCCGACTTATGG 543
 Db 3211 GAAAGTGGTATAAAGATAATCTTATGGGTCTAACAAATCATCCAGACTTAATGG 3152

Qy 544 CATGAAACCATCTCGAGCAATAACAGGATACAGCAGACGAGCAATTAGAGCAAGAG 603
 Db 3151 CATTATGTTAATTAAGACATATACTCTCTTATCCAGCAACAGCAATTAA 3092

Qy 604 ATGGCCGATAGCCCTTCTCCTTTCGCCAAGCTTAGGAACTGTGCTGCGGGG 663

Db 3091 TTGGAAGGTGAACTGATTGAACTTTCGGTTGCAAGTGCAGGCT 3032

Qy 664 GATTACTCAACTGAGGCTTGAGAGCTTATTCAGAAAGCACATGAGCC 723

Db 3031 GGATTACTCAACTGAGGCTTGAGAGCTTATTCAGAAAGCACATGAGCC 2972

Qy 724 GGGGCCATGAAACGAAAGGTTAACGCSCTTCAAATTGCAAAATGAGATA 783

Db 2971 AACATGATAGAAATGATTAGAAATGCAATTAGATGCAATTAGCTAAATA 2912

Qy 784 CCAAAGGGCGACTGATAACGAGAGAGAAATCATATAGCAATACCTCGTG 843

Db 2911 CGGATGGATGTTGACTCCGCTCATGATGCTGACAATCAGACGCTA 2852

Qy 844 ATGGCAACGAAACTGAAACTACTTCCACATATGCAATCGCAATCCAAA 903

Db 2851 ATAATTAACTACAGAACGCTTATATAGTATATGAGCTAACATAGATG 2792

Qy 904 GTAATTATTCATGAGACTGCTTGACTGTTGGACCTAAAGTGTAAAGCA 963

Db 2791 TAAAGCTCACAGTATTAAATAGAAAGATGAGCTTTAACGCTGAGA 2732

Qy 964 GAAGAGATTCATGAGCTTATA 989

Db 2731 CATATCACTTAAGAAAGTGTATGA 2706

RESULT 14

US-10-329-624-444/C
; Sequence 444, Application US/10329624
; Publication No. US20040043037A1

GENERAL INFORMATION:

APPLICANT: Charles Kunsch

Gil H. Choi

Patrick S. Dillon

Craig A. Rosen

Steven C. Barash

Michael R. Fannon

TITLE OF INVENTION: Staphylococcus aureus Polynucleotides and Sequences

NUMBER OF SEQUENCES: 256

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9110 Key West Avenue

CITY: Rockville

STATE: Maryland

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.50 inch, 1.4Mb storage

COMPILER: HP Vectra 486/33

OPERATING SYSTEM: MS-DOS version 6.2

SOFTWARE: ASCII Text

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/329,624

FILING DATE: 27-Dec-2002

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/956,171

FILING DATE: October 20, 1997

APPLICATION NUMBER: 60/009,861

FILING DATE: January 5, 1996

APPLICATION NUMBER: 08/711,986

FILING DATE: January 3, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Mark J. Hyman

REGISTRATION NUMBER: 46,789

TELECOMMUNICATION DOCKET NUMBER: PB248P1D1

TELEPHONE: (240) 314-1224

TELEFAX: (301) 309-8439

INFORMATION FOR SEQ ID NO: 444:

SEQUENCE CHARACTERISTICS:

LENGTH: 11466 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear

SEQUENCE DESCRIPTION: SEQ ID NO: 444:

US-10-329-624-444
Query Match 4 ATGTCACAGTCATGAACTGCTGACCTAACATGATAGAAAGAACATG 63

Best Local Similarity 47.5%; Pred. No. 2.9e-32; Mismatches 515; Indels 3; Gaps 1; Matches 468; Conservative 0; Missmatches 515;

Db 3688 ATGTCACAGTCATGAACTGCTGACCTAACATGATAGAAAGAACATGCTGAGCGACATG 3629

Qy 64 GATTGTCATTCTAGCTGGGGACAGGGGATTCCTATCGCGCGTTACAGCTGGAC 123

Db 3628 GATTGATTCTAGTCATGTTGGCTGAGCTAACATGATGTTGAGAA 3569

Qy 124 ATGAGACTGAGGGGGCCATAGACACAGTACGGGTATCGGTATGGGAGAAA 183

Db 3568 TCTGGACT---GGCAGCAGGGCCAAAGCCAAATGGCTTATGGCAGACAGAT 3512

Qy 184 CTGGAAATATATTTGCGACGGCATATGAAAGGGTTATCTGTGCGGCTT 243

Db 3511 ATGGAAGGTTATTTATGGTGTGTTATGACATGGCTGCCATTCAACACAA 3452

Qy 244 TATTCGGGCTATGGGGATACGGGATACAAALACGTTACGGGAGTTACCGTCACTGTC 303

Db 3451 TATTCCGGAGGTTATGATGCAATGATGACACACAAAGGGGAGGGATGAAATTAC 3392

Qy 304 CCGCMAGGTTGTCATGGCTGCTGCTGAGCTGGTGTGAGCTGGTAAAGAA 363

Db 3391 CAAGATGAAATGTCACATGGATTGGGTTACACAGGATGAGATGAA 3332

Qy 364 AAGATTGCACTTAACTGATGAACTGCAACTGACATACAGTGAAGTTACCG 423

Db 3331 CAAGCTCCAAATACATGTTGAGCTTATTAATGACATGCTGGTAAGTTCGCCA 3272

Qy 424 CTGACTGGATATGTCAGCCGGAGGGCCGAACCTGACGCCCCGACTTTATGG 543

Db 3271 TTGCATCTCATGTTCTCATGAACTGCAACTGCAATTTGCTTAAAGGGT 3212

Qy 484 GCCTCCTAACTCTATGATAATCAACCTGGTCATGACGACAGCCCCTTATGG 543

Db 3211 GAAGTGGTTAAAGATAATCTTATGGTGTCTAACATGTCAGCTTAACATGG 3152

Qy 544 CATGTAACATCTGGCAACATACAGAACTGAGCAATAGAGAGCAAGAG 603

Db 3151 CATTATGATTAATGACATATAATTTCTCTTATCCAGCAACGCAATTAA 3092

Qy 604 ATGGCCGATAGCCCTTCTCCTTCACTGGCTTTCAGCAAGCTTGGCTGCTCGGGG 663

Db 3091 TTGGAAGGTGAACTGATTGAACTATTCATGCAATTATGAGCTTGGCTGCTCGGG 3032

Qy 664 GATTACTCAACTGAGGCTTGAGAGCTTATTCAGAACTGAGTACATTGAGCT 723

Db 3031 GGATTACTCAACTGAGGCTTGAGAGCTTATTCAGAACTGAGTACATTGAGCT 2972

Qy 724 GCGCCGCGACTGATGAAAGGGTGTACGACCGCTTCAATTGGCAATATGAGATA 783

Db 2971 AACATGATAGAAATGATTAGATGCAATTATGAGCTTATTAATGAGCTTGGCTAAATA 2912

Qy 784 CCAAAGGGCGACTGATGAAAGGGTGTACGACCGCTTCAATTGGCAATATGAGATA 843

Db 2911 CGGATGGATGTCATGTCATGCTGACATGAGCTGAGCTGAGCTGAGCT 2852

Qy 844 ATGTCACAGCAACTGAGAAGCTTATTCACCACTGACATGCGCAATCCAAA 903

Db 2851 ATAATTAACTCAAGAACGTTATTAATGAGCTTATGGAGCAATGAGCTA 2792

Qy 904 GTAATTATTCATGAAAGACCTGACTGCTTGGAGCCCTAAAGTGTTCGCCA 963

Db 2791 TAAAGCTACAGATTTAATAGAAAAGATATGAGGATTAAACCTGAGAAG 2732
 Qy 964 GAGAGAGTATTCATGAGCTTAATAA 989
 Db 2731 CATATCACTATAGAAAGTGAATGA 2706

RESULT 15
 US-09-815-242-8383
 ; Sequence 8333, Application US/09/15242
 GENERAL INFORMATION:
 ; Patent No. US20020061569A1
 ; APPLICANT: Haselebeck, Robert
 ; APPLICANT: Ohlsen, Kari L.
 ; APPLICANT: Zyskind, Judith W.
 ; APPLICANT: Wall, Daniel
 ; APPLICANT: Travick, John D.
 ; APPLICANT: Carr, Grant J.
 ; APPLICANT: Yamamoto, Robert T.
 ; APPLICANT: Xu, H. Howard
 TITLE OF INVENTION: Identification of Essential Genes in
 FILE REFERENCE: ELTRIA_01A
 CURRENT APPLICATION NUMBER: US/09/815, 242
 CURRENT FILING DATE: 2001-03-21
 PRIOR APPLICATION NUMBER: 60/191, 078
 PRIOR FILING DATE: 2000-03-21
 PRIOR APPLICATION NUMBER: 60/205, 848
 PRIOR FILING DATE: 2000-05-23
 PRIOR APPLICATION NUMBER: 60/207, 727
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: 60/242, 578
 PRIOR FILING DATE: 2000-10-23
 PRIOR APPLICATION NUMBER: 60/253, 625
 PRIOR FILING DATE: 2000-11-27
 PRIOR APPLICATION NUMBER: 60/257, 931
 PRIOR FILING DATE: 2000-12-22
 PRIOR APPLICATION NUMBER: 60/269, 308
 PRIOR FILING DATE: 2001-02-16
 NUMBER OF SEQ ID NOS: 1410
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 8333
 LENGTH: 1002
 TYPE: DNA
 ORGANISM: Staphylococcus aureus
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (1) .. (1002)
 US-09-815-242-8383

Query Match 14.3%; Score 142.8; DB 3; Length 1002;
 Best Local Similarity 47.3%; Pred. No. 7.2e-32;
 Matches 466; Conservative 0; Mismatches 517; Indels 3; Gaps 1;

Qy 4 ATGTGCACAGCTTACATGGAACTCTGACCGTAAACATGATTTAGCAGAACATG 63
 Db 10 ATGTGCACAGGATTCAACTTAATAATCAGACTTCTGTGGACAGGATG 69
 Qy 64 GATTTGCACTTACAGCTGGACAGAGGTGATCTCATCCGGCTTAAGCTGGAC 123
 Db 70 GATTAATGATTATCATTAGTAGTGCTGGACAGAACATGGCTTAATGCTGGACA 129
 Qy 124 ACTGAAGCTGAGGAAAGGCCCTCAAGCACAGTACCGTTATCGGTATGGAGAA 183
 Db 130 TCTGGCACT--G3CAGACAGGCCAAAGCAGATATGGCTTATGGTACAGGAT 186
 Qy 184 CTGGAAATAATTATTCGCGGCAATTATGAAAGGGTTATCTGGGGGCTT 243
 Db 187 ATCGAAGCTTATTATGGTGTGTTATGACATGCGCTTGCCATTCAACCAA 246
 Qy 244 TATTTCGGCTATGGAGGAGACGAAAGACATACGGAGATACTGGTACATGTC 303

Db 247 TATTTCGGAGGTATAGTCATATGGCTAACACACAAAGCGATGCGATGAAATTACG 305
 Qy 304 CGCGTACGTTGACATGGGTCTGTCAGTCAGTCAGTCAGTTGGAGACGTTAAAGAA 363
 Db 307 CAAGATGAAATTGTCAGTGGATTTGGGATATAACACAGCATGAGATATGAAACAA 366
 Qy 364 AGATGCGATTTTACGATTGAGAGAAAATTAGATCTATGGATGACAGTTACCG 423
 Db 367 CAAGCATCCCATAATCATGTTGAGCTGTGATATTTAAATGATATCGGTAAGTTCGCCA 426
 Qy 424 CTTCAGTGGATATGTCAGCGGAGCGGGAAACCTGACATTCAGTGAAGTTAACG 483
 Db 427 TTGCTTATTCATGTTCCGTCAGTCACTGTTAGCTGTGATATTCAGGAGGT 486
 Qy 484 GGCCCTCAAGCTCTAGATACTACACTGCTGAGCTGGTCAAGACACAGCCCCACTTATGG 543
 Db 487 GAAGTGTATAAAGATGAAACCTTATGGTCTAACAAATCTCCAGACTTAGATGG 546
 Qy 544 CATGTAACCAATCTGCAAGAATATACAGCAAACTGACATTCAGTGAAGTTAACG 603
 Db 547 CATTATGTTATTAGACATAATCATATTCTCTTATCCGCGAACAGCAATTAA 606
 Qy 604 ATGGCGGATAGCCTTCTGCTTSCCAAGCTGGAACTGTGGTCGCGGG 663
 Db 607 TTGGAGGTTGAAAGTGTACATTCAGCAATGAGCAATTAGAGAGAGGTTGGCAGG 666
 Qy 664 GATTATAACCGCTTCCCGTTGTCAGCTGTGTTATTGAAAGACATCTAGAGCCG 723
 Db 667 GGATTTACTCACTGAGCCCTTGTAGATGGCATTTAGAAGAACAACTTGTCAA 726
 Qy 724 GCGCCGCAAAACAAAGTGTACAGCGCTTTCGAATTTCGGCAATATGAGATA 783
 Db 727 AACAAATGATAAGAAATTGGATTATGAAATGCAATTATTTAGGGAAATA 786
 Qy 784 CCAAGGGCCAGTGTAAAGGAAAGAAGAAATTCTATTAGCAATACTCTGGT 843
 Db 787 CGGATGGAATTGTCGTCATGCTGACATCTACTACATGATGACAGCGTA 846
 Qy 844 ATGTCACAAACTGGAAACTACTATTCCACCACTATGAAATCGGCAATCCAAA 903
 Db 847 ATAATTTAACTACAGAACTGTTATTAAGTATTATGGCAGCAATGAAATAGCA 906
 Qy 904 GAAATTATTTCTGAGACCTCTGCTTGGAGCTTAAGGTTTCGCTAAAGCA 963
 Db 907 TAAAGCTCACAGATGTTATTAAGAAGATGACGATTATGGCAGCAATGAAATAGCA 966
 Qy 964 GAGAGAGTATCAGGCTTAATAA 992
 Db 967 CATATCACTATTAAGTGAATGA 992

Search completed: March 18, 2006, 13:28:30
 Job time : 998 secs

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GenCore version 5.1.7

Sequence 348226,
Sequence 82, Appl

OM nucleic - nucleic search, using sw model

Run on: March 18, 2006, 11:54:08 ; Search time 452 Seconds

(without alignments)
5138.006 Million cell updates/sec

Title: US-10-812-387-1

Perfect score:

996

Sequence: 1 catatgtgcacaaggctttac.....atgagcttaattaaggatcc 996

Scoring table: IDENTITY NUC Gapext 1.0

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Maximum Match 100%

Searched: 8023312 seqs, 1165852854 residues

Total number of hits satisfying chosen parameters: 16046624

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0*

Listing first 45 summaries

Database : Published Applications NA New:*

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2: /cgtn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*

3: /cgtn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

4: /cgtn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*

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8: /cgtn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*

9: /cgtn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

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11: /cgtn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

12: /cgtn2_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*

13: /cgtn2_6/ptodata/1/pubpna/US12_NEW_PUB.seq:*

ALIGNMENTS

RESULT 1

US-10-793-626-413
; Sequence 413, Application US/10793626

; Publication No. US2005055478A1
; GENERAL INFORMATION:

; APPLICANT: KIMMELY, WILLIAM JOHN

; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEARIC ACIDS AND PROTEINS

; FILE REFERENCE: PUS360US

; CURRENT APPLICATION NUMBER: US/10/793-626

; PRIOR APPLICATION NUMBER: 6/164,258

; PRIOR FILING DATE: 1999-11-09

; SOFTWARE: Patentin Ver. 2.1

; NUMBER OF SEQ ID NOS: 4472

; SEQ ID NO: 413

; LENGTH: 990

; TYPE: DNA

; ORGANISM: Artificial Sequence

; FEATURE: OTHER INFORMATION: Description of Artificial Sequence: synthetic

; OTHER INFORMATION: nucleic acid sequence

US-10-793-626-413

Query Match 16.0%; Score 159; DB 8; Length 990;
Best Local Similarity 49.8%; Pred. No. 2e-35;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Sequence 413, APP
Sequence 4184, APP
Sequence 367, APP
Sequence 369, APP
Sequence 58863, APP
Sequence 58863, APP
Sequence 29311, A
Sequence 392869, Sequence 392869,
Sequence 654182, Sequence 654183,
Sequence 2969, APP
Sequence 2969, APP
Sequence 102, APP
Sequence 392868, Sequence 392868,
Sequence 45228, APP
Sequence 45228, APP
Sequence 45229, APP
Sequence 45229, APP
Sequence 45230, A
Sequence 45230, A

Qy 62 TGGATTTGCAATTCTACGTCAGTGTCTATCGCGCGTACAGCTGA 61
8 ATATGTTGACTGCATTCTTATATAAACACACGTTACCATTTAGTAGACA 67
Db 68 TGGATTTGCAATTCTACGTCAGTGTCTATCGCGCGTACAGCTGA 121
Db 182 RACTTGAAATAATTATTTCGCGCATTATGAAAGCGGTTTCTCTGCGCGC 241
185 AGTGGACGCTATAGTTGATGATGATACGAAAGGTTACGTTTCGAC 244

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. Score Query Match Length DB ID Description

1 159 16.0 990 8 US-10-793-626-413
Sequence 413, APP
Sequence 3345, APP
Sequence 4184, APP
Sequence 367, APP
Sequence 369, APP
Sequence 58863, APP
Sequence 58863, APP
Sequence 29311, A
Sequence 392869, Sequence 392869,
Sequence 654182, Sequence 654183,
Sequence 2969, APP
Sequence 2969, APP
Sequence 102, APP
Sequence 392868, Sequence 392868,
Sequence 45228, APP
Sequence 45228, APP
Sequence 45229, APP
Sequence 45229, APP
Sequence 45230, A
Sequence 45230, A

QY 242 TTATTTCGGGCTATCGGGAGTACGAAACGATACTGGGAGAACATCCGTCATCG 301
Db 245 ATTRACTCACTGGGAGCCTCACTAGTACCATTAACGTTATGTTAATTCTAG 304
QY 302 TCCCGCMGAGTTTGACATGGGTGCTCAGTCAGTCITTTGAGAACGCTAAAG 361
Db 305 CACCTGAGGAGTTATGTTGGGTTAGTTTAAAGTATTAACGCTTACGCTTAAAC 364
QY 362 AAAAGATTCGATTTACGATGAGGAAAAATTAGATCTATGCTATGCTACGTTAAC 421
Db 425 CTTTACATTCATGGTCACTGATGAAACAGGACATACGGTAGCTAGAACCTCAC 424
QY 365 AAAGAGTTAAGAAATATCATATTATGAAATGAAAGAACAAATACGACTTGAAAT 424
Db 422 CGCTTACTGGATATGTCAGACGGACCGGCCAACCTGACGATAGAACAGAGCG 481
QY 482 ACGGCCTGAGGCTATGATAATCACCTGGTGTATGAGAACAGCCCACITATAT 541
Db 485 GCTTATTATGATAAGATAATATGTTACATCCCTAACATGAACTAAATTAGTT 544
QY 542 GCGATGAAACCATCTGAGCAATATACAGGATTCAGCGGAAGCAATTAGAGCGAAG 601
Db 545 GSCATCTATCTAATCTAATGAAATTAACGCTTTTAAACGCCAACAGAAATCACCAT 604
QY 602 AGATGGGGGATGGCCCTTCCTGGCGGAGCTTAGGACTGGGCTGAGCAGAAC 661
Db 605 TAATAGTAAAGTGTCACTGAGATOAATGGGCTGTAAGCAGAACAAATGGCTAC 664
QY 662 GGGATATAACACGCCCTTCGGGTTGTCAGAGCTGTATTGAGAACACATCTAGAGC 721
Db 665 GGGTTATACGTCACAGATCGTTATACGGCTACATTTAGAACACCACTACCT 724
QY 722 CGCGGGCATGAAACGAAAGGTTACAGCCSCTTCAATTTCGCAATTATGAGCA 781
Db 725 GTCGCCATATGAGATGAAATTTATGAAATTGTTAAGTGTCTAGATCAGTCAGTA 784
QY 782 TACCAAGGGCGATGTAACGGAGAACGAAATCTATACGCAATATACCTTCGG 841
Db 785 TCCTCTAACGGTGCAGTTAT--CGATGCCATATAATACATACACATATCATAG 841
QY 842 TGATGTGCACAGAACACTACTATTCACCACTATGAGAACATCGCAATCCCAA 901
Db 842 TGATGTGCACAGAACACTACTATTCACCACTATGAGAACATCGCAATCCCAA 901
QY 902 AAGTAATTATTCATGA 920
Db 902 AAATAAAATTAACGGAGA 920

RESULT 2
US-10-793-626-3345/C
; Sequence 3345, Application US/10793626
; Publication No. US20050255478A1
; GENERAL INFORMATION:
; APPLICANT: KIMMEL, WILLIAM JOHN
; TITLE OF INVENTION: STAPHYLOCOCCUS EPIDERMIDIS NUCLEIC ACIDS AND PROTEINS
; FILE REFERENCE: PUS480US
; CURRENT APPLICATION NUMBER: US/10/793, 626
; CURRENT FILING DATE: 2004-03-04
; PRIORITY APPLICATION NUMBER: 60/1164, 258
; PRIOR FILING DATE: 1999-11-09
; NUMBER OF SEQ ID NOS: 4472
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3345
; LENGTH: 2975
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: synthetic
; OTHER INFORMATION: nucleic acid sequence
; US-10-793-626-3345

RESULT 3
US-10-793-626-4184
; Sequence 4184, Application US/10793626
; Publication No. US20050255478A1
; Best Local Similarity 49.8%; Pred. No. 3 4e-35;
; Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

QY 1755 ATATGTCACAGTCCTTACATGAAACTGCTGACCGTAAATGTTAGCAGAACAA 121
Db 1695 TGGACTTGTCAATTGAAATTAAATGTTATCCTACCATGTTACGCCATTATCACC 1636
QY 122 ACAGTGAAGCTACGGGAAGGGCCATCAGACAGTAGCGGTATCGTATGGGAGAA 181
Db 1578 ACTTGGAAATATTATGTTGCGACGCAATTGAAATACGAAAGAACAACTTAC 1519
QY 242 TTATTTCGGCTATGGGAGTACGAAACGATACTGGGAGAACATCCGTCATCG 301
Db 1518 ATTRACTCACTGGGAGCCTATGAACTTACGCTACATACGTTATGTTTACCTAG 1459
QY 302 TCCCGCMGAGTTTGACATGGGTGCTCAGTCAGTCITTTGAGAACGCTAAAG 361
Db 1458 CACCTGAGGAGTTATGTTGGGTTAGGTTAATGAACTTACGTTAGGAAATTAAC 1399
QY 362 AAAGAGTTGATCTTACGATGAGAACGAAATTAGATCTATGGGATACGTTAC 421
Db 1398 AAAGGTAAAGAAATCATATATATGAGTAAAGAACAAATAGCTTACGTTAGGAAATTAAC 1339
QY 422 CGCTTACTGGATATGTCAGACGGACGGACGGGAAACCTGAGATAGAACAGAGCG 481
Db 1338 CTTCATCTTCATGTCAGTCACTGATGAAACAGGAAATACCCATAGCAGCTCACATG 1279
QY 482 ACGGCCTGAGGCTATGATAATGAACTATGAGAACATGGGTCTGAGGAACTTAT 541
Db 1278 GTTATTAAATGTAAGTAAATTATGTTACACTTAAACATGAAATGAAATTAATGATT 1219
QY 542 GCGCTGTGAACTCTGCGAGCAATACGGGAACTGGGTCTGAGGAAAGCCGCACTTAT 601
Db 1218 GCGACATCTAATTTAAAGAAATTAGCTTAAACGGCAACGAAATGGAGCAAG 1159
QY 602 AGATGGGGGATGGCCCTTCCTCTTGGCAAGGCTTACGAAACTGTTGCTCGGCCG 661
Db 1158 TAATAGTAAAGTGTCACTGAGATCAATGGCTGAGCAGAACAAATGGCTACCG 1099
QY 662 GGGATTATACACCCCTTCGGGTTGTCAGAGCTGTATTGAGAACACCTAGAGC 721
Db 1098 GTGGTTATACGTCACAGATCGTTTACGCGTACATTTAGAACACCACTACGCT 1039
QY 722 CGGGGCCATGAAACGAAAGGTTAACGGCGCTTCAATTGCGAAATATGAGCA 781
Db 1038 GTTCCATATGAGATGAAATTATGAAATTGTTAGTCTAGATCAGTCAGTCAGTA 979
QY 782 TACCAAGGGCGATGTAACGGAGAACGAAATCTATACGCAATATCTCCG 841
Db 978 TCCTCTAACGGTGCAGTTAT--CGATGCCATATAATACATACACATATCATAG 922
QY 842 TGATGTGCACAGAACACTACTATTCACCACTATGAGAACATCGCAATCCCAA 901
Db 921 TGATGTGCACAGAACACTACTATTCACCACTATGAGAACATCGCAATCCCAA 862
QY 902 AAGTAATTATTCATGA 920
Db 861 AAATAAAATTAACGGAGA 843

APPLICANT: KIMMERLY, WILLIAM JOHN
FILE REFERENCE: PUS480US
CURRENT APPLICATION NUMBER: US 10/793, 626
CURRENT FILING DATE: 2004-03-04
PRIORITY FILING DATE: 1999-11-09
NUMBER OF SEQ ID NOS: 4472
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO: 4184
LENGTH: 4114
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: synthetic
US-10-793-626-4184

Query Match Best Local Similarity 16.0%; Score 159; DB 8; Length 4114;
Matches 458; Conservative 0; Mismatches 455; Indels 6; Gaps 2;

Qy 2 ATATGTCACCAAGCTTACTTGAACTCTGACCGTAACTGTAGCAGAGCAA 61
Db 1626 ATATGTTGACTGGCATTTTATACAAACAGCTTACAGTAACTGTAGCAGAGCAA 61
Qy 62 TGGATTTCGATTCACTGCTTACAGCTGGGACAGAGGTGTTCTTAACCGCCGTTACAGCTGA 121
Db 1686 TGACTTCTGATTGAAATTATGTTATCCAAACATGTTCCACGCCATTACACTACC 1745
Qy 122 ACAGTGAAGCTGACGGAAGGCCATCACACAGTACGGTTATCGTATGGGAGAA 1685
Db 1746 AATTGATCTAGTCAGAACATGGCTT--GATATGTTGTTGACAATTTAA 1802
Qy 182 AACCTGGAATAATTATGCGACGGCATTAATGAAAGGGTTATCTGTGGGGC 241
Db 1803 AAGTAGGAGCTTATGATTTGTTGATGTTAAGCAGAAAGTTTACATTCTGAACT 1862
Qy 242 TTATTTCCGGCTATGGGGAGTACGAAAAAAAGATAACGGGAGATACGGTCACATG 301
Db 1863 ATTACTTCACTGTCGAACCTCATACATACCCATAAACGTTAGTTGTTTACTAG 1922
Qy 302 TCCCGCAGTGTGTTGACATGGCTGCTACTGTCAGTCTTGGAGAGCTAAAG 361
Db 1923 CACCTGAGGAGTTATGTTGGTTAGTTAAAGTATTAGCCGAAATTAAAC 1982
Qy 362 AAAGATTCGATCTTAACTGTTAGAAGAAATTAGATCTTGGATACGTTAC 421
Db 1983 AAAGGTTAGAARATCAATTATGAACTTAACTGACTTTGATATGTTCTC 2042
Qy 422 CGCTTCACTGATATGTGACGACGGACGGCGGAACCTGAGATAGAACCCAGAGCG 481
Db 2043 CTTTACATTTCTGTCACTGTTAGTAACTGAACTTAACTAAATTAGATT 2102
Qy 482 ACGGCTCTCAAGCTCTATGATTAATCAACTGTCATGACAGCCGCCTTAT 541
Db 2103 GCTTATTATAGTAAAGATAATTATGTTACCTTAACTAAATTAGATT 2162
Qy 542 GCGATGTAACATCTGAGCATATACAGGATCAGGCCGAGCAATTAGAGCAAG 601
Db 2163 GGCATCTATCTAACTAAGAATTACGCTTTCAGCCACGAAATCACCACAT 2222
Qy 602 AGATGGGGATTAGCCCTTCGCTTGTGCAAGGTTAGAACCTGTTGCTGCGG 661
Db 2223 TAATAGTAAAGCTGACTTAACTGAACTTAACTTAACTTAACTTAACT 2282
Qy 662 GGATTATAACCGCCCTTCGGTTGCAAGCTGTTATGAAAGAACATCTAGAGC 721
Db 2283 GTOGTATAGTCAACAGATCGTTATAGCCCTACATTTAGACACCACTAGCT 2342
Qy 722 CGCGCGCGGATGAAACGAAAGGTTAACGGCCCTTCAAAATTGCAATATGAGA 781
Db 2343 GTTCCCCATAATGAGATGAAATTATGATGTTTAAGTCTAGAACTCAGTCAGTA 2402

RESULT 4
US-11-074-176-367
Sequence 367, Application US/11074176
Publication No. US20050250135A1
GENERAL INFORMATION:
APPLICANT: Klaenhammer, Todd R.
APPLICANT: Russell, William M.
APPLICANT: McAuliffe, Olivia
APPLICANT: Peril, Andrea Accurate
TITLE OF INVENTION: Nucleic Acid Sequences Encoding
TITLE OF INVENTION: Stress-Related Proteins and Uses Thereof
FILE REFERENCE: 5051-694
CURRENT APPLICATION NUMBER: US/11/074, 176
CURRENT FILING DATE: 2005-03-07
PRIORITY FILING DATE: 2004-03-08
NUMBER OF SEQ ID NOS: 381
SOFTWARE: Fast-SEQ for Windows Version 4.0
SEQ ID NO: 367
LENGTH: 975
TYPE: DNA
ORGANISM: Lactobacillus acidophilus
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(975)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(10)
OTHER INFORMATION: ORF 892; bshA
US-11-074-176-367

Query Match Best Local Similarity 9.3%; Score 93; DB 12; Length 975;
Matches 340; Conservative 46.4%; Pred. No. 2e-16; Mismatches 390; Indels 3; Gaps 1;

Qy 197 TATTGCGACGCGCATTTATGAAAGCGCTTATCTTGCGCGCTTATTCGGGCT 256
Db 188 TATTTGCGCTTACATGAAAGGTTTGTATGGCTTGGCGACACTTCACCTCAGGAA 247
Qy 257 ATGGGGGTACCGAAACGATACGGGAGATACCGTCACATTGRCGGCATGAGCTTG 316
Db 248 ATGCTACATATTATGAAAGAA---GAAATTAAAGTAATATTGCTTCCTTGAATCA 304
Qy 317 TGACATGGTGTGTCGCTCTGAGTCTTGGAGAGCTTAAGAAAGATCAGTCACTT 376
Db 305 TCCCTGGTGTGTCGCTCTGAGTCTTGGAGAGCTTAAGAAAGATCAGTCACTT 364
Qy 377 TAACGATGTTAGAAGAAATTAGATCTATGATAGCTTACCGCTTACTGGATAT 436
Db 365 TCAACATGGCGATTAAATTGAGCAAAATGCAAGCTCTTCACGGTTA 424
Qy 437 TCTCAGCGGACGGCGCGAAACCTGAGTAAAGACACAGAGCGAGGGCCCTAACAGCT 496
Db 425 TGGAGTAAACAGGATACATCATTTAGTGTGAAACAGACAAGATGGAACTTCAATT 484
Qy 497 ATGATATCAACCTGTTGTCAGTACGAGCAACGCCCGACTTATGCACTTACCATC 556
Db 485 ATGATATCCAGTGGCTGTTAAGTCTAGAACTTAACTCCACATTCATTCAATT 544

QY 557 TGCAGCAATACTACAGGAATCTGACCGAAGGATTAGAGACCAAGAGATGGCGGATTTAG 616
Db 545 TAATAACTAATGCTGAGTATCTCCAAAATGCTAAATACTTCAGATAAGTA 604
QY 617 CCCCTTCTGTGTTGCCAANGCTTAGAACCTGCTGGTCCTCCGGGGATATACACCGC 676
Db 605 ATATGCTGGCTACAGCCGTTGAGGTTCTACACTTACACCTTACAGGTGGATGGATTCTG 664
QY 677 CTTCGGTTGTCAGAGCTTTATTGAGAGAACATCTAGAGCGGGCGGAGAA 736
Db 665 ATACAGTTTGTCAGAGCTCTTCATAAATTAAATTGTCCTCAATTGCGAACCGAG 724
QY 737 CGAAAGGTGTRACASCGCTTTCATAATTGCGAACATATGCACTAACCGAG 796
Db 725 AGAAATAATTGATACTTACTTACATTCACATTACATCGGTGACACACAAAGGACTGG 784
QY 797 TGATACAGGAAAGGAAATTATAGCAATTGCAATTCTCGTGTGCAACGAAA 856
Db 785 ATGAAGTTGCGTCAACTCATTTGATGATACATTGAGACTTAATTGACA 844
QY 857 CTGGAAGACTACTATTCCACCACTATGACATCGGAATTCAAAGATTAATTTC 916
Db 845 AGGTTTCTACTACACCCTATCACAACAAATTACCTGTTGATGATA 904
QY 917 ATGAAGACCTGAA 929
Db 905 AGAAGAGATCTGA 917

RESULT 5
US-11-074-176-369
; Sequence 369, Application US/11074176
; Publication No. US20050250135A1
; GENERAL INFORMATION:
; APPLICANT: Klaenhammer, Todd R.
; APPLICANT: Russell, William M.
; APPLICANT: Altermann, Eric
; APPLICANT: McAluliffe, Olivia
; APPLICANT: Peril, Andrea Aizcarrate
; TITLE OF INVENTION: Nucleic Acid Sequences Encoding
; FILE REFERENCE: 5051-694
; CURRENT APPLICATION NUMBER: US/11/074,176
; PRIOR APPLICATION NUMBER: 60/551,161
; PRIOR FILING DATE: 2004-03-08
; NUMBER OF SEQ ID NOS: 381
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 369
; LENGTH: 975

TYPE: DNA
ORGANISM: Lactobacillus acidophilus
FEATURE: NAME/KEY: CDS
LOCATION: (1) . . . (975)
FEATURE:
NAME/KEY: misc_feature
LOCATION: (0) . . . (0)
; OTHER INFORMATION: ORF 1078; bbbb

US-11-074-176-369
Quary Match 8.4%; Score 83.8; DB 12; Length 975;
Best Local Similarity 45.4%; Pred. No. 8 9e-14; Mismatches 407; Indels 3; Gaps 1;
Matches 341; Conservative 0; Mismatches 407; Indels 3; Gaps 1;

QY 181 AACTTGGAAATATATTGCGCGGCAATTGAAACGGTTATCTGGCGG 240
Db 172 ATGATGATTATCCATTATGTCGATTAATGAAAGGGCTTGGATTGCGGA 231
QY 241 CCTTATTCGGCTATGGGAGTACAAAGATACGGAGATACCCCTACATT 300
Db 232 TTAATTTCAGG--TCCTAATCATTAATCTCTAAATCGAAGGTTAAGGAAATT 288

QY 301 GTCCCGCATGAGTTGTCATGGTGTCTCAGTCCTTGAGAGGTTAAA 360
Db 289 GCTCTTTGAAATTATGCCATACTTATTAAGTAATTCAGCTGTTAA 348
QY 361 GAAAGAGATGCGCTTTAGAGTTGAGAAGAAATTAGATCTTGGATACAGTTTA 420
Db 349 GAAATCTAGATATGCAAAATTTAAATATAGCTTTCAGCAATTATCTGCGCT 408
QY 421 CGCTTCTACTGGATATTTCAGACGGCGGGCGGAACCTGAGATGAAACCGAGCA 480
Db 409 GATTTACATGGATTAGTGTAAAGCTGTTAGACTGTTAGACTACCAT 468
QY 481 GACGCCCTCAAGCTCTATGATAATCAACCTGGTGTCTAGACAGACGCCGACTTTA 540
Db 469 TCAGGTTACATATTAGTGTAACTTCCAGTGTACTACACTACCTGAAATTCCG 528
QY 541 TGGTAGTGTACCACTTSCAGCATATACAGGATCACCGAGAACAGAGCAA 600
Db 529 GATCATTATTAATTAATTAGTGTACTACCGCGAGTTACTCCAGATAATCTGAGATA 588
QY 601 GAGATGGGGAGTAGCCCTTGCTTGGCCAAGGTTAGAACCTGGTGTGCG 660
Db 589 TTGGTCTCTATGTTGATCTATATAGTAGAGGCTTAGTGTGCTGAG 648
QY 611 GGGGATTATACACGCCCTCCCGGTTCTAGACCTGTTTGAAGAACATCTAGAG 720
Db 649 GTGGAAATGGATCTAGCTCTGATTCAGTTAGTAGCTTGTGCAACACTCA 708
QY 721 CCGCGGGGATGAAACGAAAGGTTACAGCCCTTCAAAATTGCAATAGCG 780
Db 709 CAAGGAAATAATGAGTGGAAATGTTCTAAATTATTCATATTCGATGAA 768
QY 781 ATACCAAGGGCGAGTGTAACTGAAAGAGAAATTCACTTACCCAAATACTTC 840
Db 769 CAACCTGATGTTAGATGAGTAGAGAAATACTGATACATGATAGATAGAT 828
QY 841 GTGATGTCGAGAACCTGGAAACTACTTCCACCTATGAAATGGCAATATCCAA 900
Db 829 TGTGAGACTGTAGATAAGSTATTGTTGACTTACTCTATGACAATATGGATTAA 888
QY 901 AAAGTAAATTATTCATGAGACCTTACT 911
Db 889 GCAGTGTGATGCTAAAGCAGATTAGTT 919

RESULT 6
US-10-750-185-59863/c
; Sequence 59863, Application US/10750185
; Publication No. US20050260603A1
; GENERAL INFORMATION:
; APPLICANT: MMi GENOMICS, INC.
; APPLICANT: DENISE, Sue K.
; APPLICANT: KERR, Richard
; APPLICANT: ROSENFIELD, David
; APPLICANT: HOLM, Tom
; APPLICANT: BATES, Stephen
; APPLICANT: FANTIN, Dennis
; TITLE OF INVENTION: COMPOSITIONS FOR INFERRING BOVINE TRAITS
; FILE REFERENCE: MMi1.00-2
; CURRENT APPLICATION NUMBER: US/10/750,185
; CURRENT FILING DATE: 2003-12-31
; PRIOR APPLICATION NUMBER: US 60/437,482
; PRIOR FILING DATE: 2002-12-31
; NUMBER OF SEQ ID NOS: 64922
; SOFTWARE: PatentIN version 3.1
; SEQ ID NO: 59863
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Bovine 19866881284323
; US-10-750-185-59863
Query Match 3.9%; Score 38.8; DB 8; Length 720;

TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
 TITLE OF INVENTION: Nucleotide Polymorphisms in the Human Genome
 FILE REFERENCE: 108927-135
 CURRENT APPLICATION NUMBER: US/09/925, 065A
 CURRENT FILING DATE: 2001-08-08
 PRIOR APPLICATION NUMBER: US 60/243, 096
 PRIOR FILING DATE: 2000-10-24
 PRIOR APPLICATION NUMBER: US 60/252, 147
 PRIOR FILING DATE: 2000-11-20
 PRIOR APPLICATION NUMBER: US 60/250, 092
 PRIOR FILING DATE: 2000-11-30
 PRIOR APPLICATION NUMBER: US 60/261, 766
 PRIOR FILING DATE: 2001-01-16
 PRIOR APPLICATION NUMBER: US 60/289, 846
 PRIOR FILING DATE: 2001-05-09
 NUMBER OF SEQ ID NOS: 957086
 SOFTWARE: FastSEQ for Windows Version 4.0
 SEQ ID NO: 654182
 TYPE: DNA
 ORGANISM: Homo sapiens
 US-09-925-065A-654182

RESULT 11
 Query Match 3.6%; Score 35.4; DB 6; Length 419;
 Best Local Similarity 57.8%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;
 Matches 63; Conservative 0; MisMatches 46; Indels 0; Gaps 0;

Qy 333 AGTCCTGCACTTGTGAGAACGTTAAAGAAAGATTGATCTTAAACGATTTGAGAGA 392
 Db 244 AGATTAGCATGATTAGAACAGATAATTAGATAACTGACCATTTATGGAA 303

Qy 393 AAATTAGATCTTGTGAGAACGTTAAACGATTTACCCCTCACTGGATATGTC 441
 Db 304 TAATTAGATGAACTGAACTGTTCTCCACTCTGTAATTGTTA 352

RESULT 12
 Query Match 3.6%; Score 35.4; DB 7; Length 5901;
 Best Local Similarity 50.9%; Pred. No. 19; Mismatches 81; Indels 0; Gaps 0;
 Matches 84; Conservative 0; MisMatches 81; Indels 0; Gaps 0;

Qy 693 AGCGTTTATTGAGAACATCTAGAGCCGGCCATGAAACGAAGGTTAACGCC 752
 Db 894 AGCTTATACACGATGAAATGTTGATTCGCTACAGGTSAGGTAAACACA 953

Qy 753 CGCTTTCATTTGGAAATGACCATACCCAGGCGCAGTGATRACGGAGAGA 812
 Db 954 CGTGCACTTACTAGATAACACCGTAAACAGTCTCGTGTGCAACGAAAC 857

Qy 813 CGAAATTCTTATACGAAATACCTCTCGTGTGCAACGAAAC 1013
 Db 1014 CGAAATTCTTATACGAAATACCTCTCGTGTGCAACGAAAC 1058

RESULT 13
 Query Match 3.6%; Score 35.4; DB 7; Length 5901;
 Best Local Similarity 50.9%; Pred. No. 19; Mismatches 81; Indels 0; Gaps 0;
 Matches 84; Conservative 0; MisMatches 81; Indels 0; Gaps 0;

Qy 333 AGTCCTGCACTTGTGAGAACGTTAAAGAAAGATTGATCTTAAACGATTTGAGAGA 392
 Db 244 AGATTAGCATGATTAGAACAGATAATTAGATAACTGACCATTTATGGAA 303

Query Match 3.6%; Score 35.4; DB 7; Length 5901;
 Best Local Similarity 50.9%; Pred. No. 19; Mismatches 81; Indels 0; Gaps 0;
 Matches 84; Conservative 0; MisMatches 81; Indels 0; Gaps 0;

Qy 693 AGCTTATTGAGAACATCTAGAGCCGGCGCCATGAAACGAAGGTTAACG 752
 Db 894 AGCTTATACACGATGAAATGTTGATTCGCTACAGGTCAGGTAAACAGA 953

US-10-932-182A-2969
 Sequence 2969, Application US/10932182A
 Publication No. US200606046253A1
 GENERAL INFORMATION:
 APPLICANT: NAKAMURA, NORIHIKO
 APPLICANT: KODAMA, YUKIKO
 APPLICANT: FUJIMURA, TOMOKO
 APPLICANT: ASHIKARI, TOSHIHIKO
 TITLE OF INVENTION: METHODS FOR ANALYZING GENES OF INDUSTRIAL YEASTS
 FILE REFERENCE: 030085-043
 CURRENT FILING DATE: 2004-05-02
 NUMBER OF SEQ ID NOS: 197023
 SOFTWARE: Patentin version 3.3
 SEQ ID NO: 2969
 LENGTH: 5901
 TYPE: DNA
 ORGANISM: Saccharomyces pastorianus
 US-10-932-182A-2969

Query Match 3.6%; Score 35.4; DB 6; Length 419;
 Best Local Similarity 57.8%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;

Qy 333 AGTCCTGCACTTGTGAGAACGTTAAAGAAAGATTGATCTTAAACGATTTGAGAGA 392
 Db 244 AGATTAGCATGATTAGAACAGATAATTAGATAACTGACCATTTATGGAA 303

Query Match 3.6%; Score 35.4; DB 6; Length 419;
 Best Local Similarity 57.8%; Pred. No. 5.1; Mismatches 0; Indels 0; Gaps 0;

Qy 333 AGTCCTGCACTTGTGAGAACGTTAAAGAAAGATTGATCTTAAACGATTTGAGAGA 392
 Db 244 AGATTAGCATGATTAGAACAGATAATTAGATAACTGACCATTTATGGAA 303

Query Match 3.6%; Score 35.4; DB 7; Length 5901;
 Best Local Similarity 50.9%; Pred. No. 19; Mismatches 81; Indels 0; Gaps 0;

Qy 693 AGCTTATTGAGAACATCTAGAGCCGGCGCCATGAAACGAAGGTTAACG 752
 Db 894 AGCTTATACACGATGAAATGTTGATTCGCTACAGGTCAGGTAAACAGA 953

Page 7

Qy	753	CGGTTTCAATTGCGAAATATGCCATACCAAGGGCAGTGATAACGGAGA	812
Db	954	CGTGTGACTACTATAGGATATTAACCGTTAACAGTTCTCGTGATCACAGGARAA	1013
Qy	813	CGAAATTCTTATAGCAATACTTCCTGATGTGCAACGAAC	857
Db	1014	CGAAATTGATATACATACGATAGTTCAAGTTGTCAGTAGTGC	1058

PRIOR FILING DATE: 2001-01-16
; PRIOR APPLICATION NUMBER: US 60/289,846
; PRIOR FILING DATE: 2001-05-09
; NUMBER OF SEQ ID NOS: 957086
; SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 392868
; LENGTH: 583
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-925-065A-322868

REASON: 14
US-11-072-175-102
Sequence 102, Application US/11072175
Publication No. US2006002994A1
GENERAL INFORMATION:
APPLICANT: Bristol-Myers Squibb Company
TITLE OF INVENTION: IDENTIFICATION OF GENES FOR PREDICTING ACTIVITY OF COMPOUNDS THAT INTERACT WITH AND/OR MODULATE PROTEIN TYROSINE KINASES AND/OR TITLE OF INVENTION: PROTEIN TYROSINE KINASE PATHWAYS IN BREAST CELLS
FILE REFERENCE: D0273A CTP
CURRENT APPLICATION NUMBER: US/11/072,175
CURRENT FILING DATE: 2005-03-05
PRIORITY APPLICATION NUMBER: US 60/406,385
PRIORITY FILING DATE: 2002-06-27
PRIORITY APPLICATION NUMBER: US 10/648,593
PRIORITY FILING DATE: 2003-08-26
NUMBER OF SEQ ID NOS: 571
SOFTWARE: PatentIn version 3.2
SEQ ID NO 102
LENGTH: 961
TYPE: DNA
ORGANISM: Homo sapiens
US-11-072-175-102

Query Match	Score	DB	Length
Best Local Similarity	3.5%	49,74;	DB 6;
Matches 88; Conservative	49,74;	pred. No. 0;	Mismatches
Qy	89;	Indels	0;
Qy	802	ACGGAGAGGAGCAATTCAATAGCAATTACTTCGGATGTCGAACGAACTTGA	861
Db	341	ATGGAGAAGGCTTAATGATGATATGCAAGAAGAAGAACATCTGAAAGACTCATA	282
Qy	862	AACATCATATTCCACCRCTATGACAATCGGAAATCTAAAGATTAATTATTCTGTGAA	921
Db	281	CTGATATGATTCACATATGACATTCAGAAACAAACACCAGTGAAATGAA	222
Qy	922	GACCTGACTGTGTTGGCTTAAGGTTTCGGTTAACCGAGAGAGAGATCT	978
Db	221	GATCAGGTTGCCAAGGAAACCGGGRRGAACGGTGGCCACAGGAGATCT	165

Query	Match	Best Match	Similarity	Score	DB	Length
Qy			3.5%	35	DB 9;	Length 961;
Db	TTACATGTCGGCATGAGTTGTGAATGGGTGCTCGTCACTGTCAGTTGGAG	TTAACAGGTCCATGAAAGTGTGCTCTGTGATGATGCTGTCGCTGGCTGGAAACC	47.1%	352		
Qy	ACGTAAGAAAGAATGATCGATCCTAACGATGTTAGAAAAAATAGATCTATTGATA	AGGGAGCAGCAACTATTCGAGATGTTCTGTGTTCACTGAAAAAATCTATTTCATTGAGA	46.6%	412		
Db	353	526	5.2%	585		
Qy	CAGTTTACCGTTCACTGGATTTGTCAGACCGGACGGGCCAACCTGACGATGAC	CAGAGCGACGCGCTCAAGTCTATGATTAATCACCTGTTGTCATGAAATACCCCTTAGGAA	41.3%	472		
Db	586	646	5.8%	645		
Qy	473	646	4.7%	519		
Db	CHAGAGCGACGCGCTCAAGTCTATGATTAATCACCTGTTGTCATGAAATACCCCTTAGGAA	ATAAGAATACCTGGCAAAATAGAGAACGAACTGACGGTTAG	6.4%	692		

US-09-925-065A 332868/C
Sequence 392868, Application US/09925065A
Publication No. US20040181048A1
GENERAL INFORMATION:
APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide Polymorphisms in the Human Genome
FILE REFERENCE: 10687-135
CURRENT APPLICATION NUMBER: US/09/925, 065A
CURRENT FILING DATE: 2001-08-08
PRIOR APPLICATION NUMBER: US 61/243, 096
PRIOR FILING DATE: 2000-02-24
PRIOR APPLICATION NUMBER: US 60/252, 147
PRIOR FILING DATE: 2000-11-20
PRIOR APPLICATION NUMBER: US 60/250, 092
PRIOR FILING DATE: 2000-11-30
PRIOR APPLICATION NUMBER: US 60/261, 766